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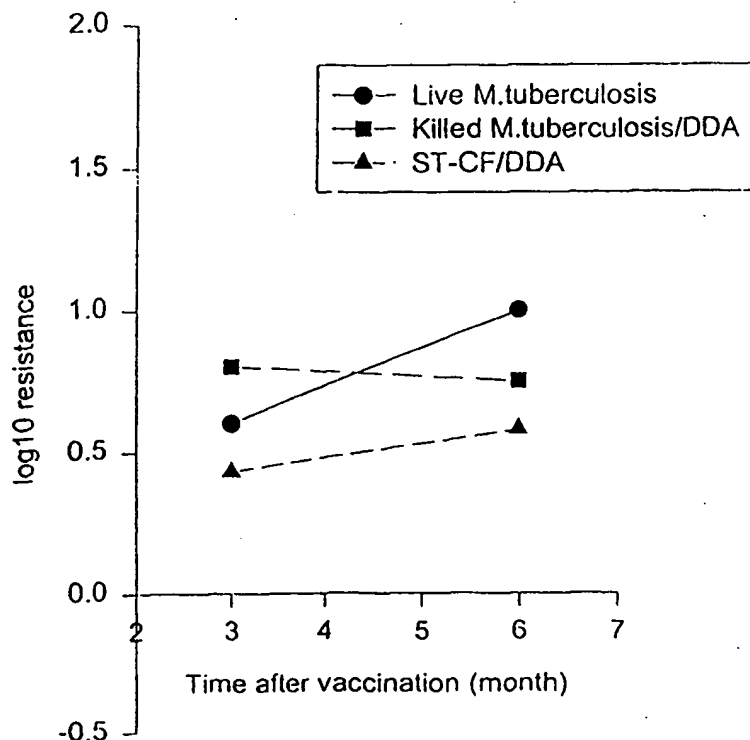
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(54) Title: TB VACCINE AND DIAGNOSTIC BASED ON ANTIGENS FROM THE *M. TUBERCULOSIS* CELL

(57) Abstract

The present invention relates to substantially pure polypeptides, which has a sequence identity of at least 80 % to an amino acid sequence disclosed, or which is a subsequence of at least 6 amino acids thereof, preferably a B- or T-cell epitope of the polypeptides disclosed. The polypeptide or the subsequence thereof has at least one of nine properties. The use of the disclosed polypeptides in medicine is disclosed, preferably as vaccine or diagnostic agents relating to virulent *Mycobacterium*. The invention further relates to the nucleotide sequences disclosed and the nucleotide sequences encoding the disclosed polypeptides. Medical and non-medical use of the nucleotide sequences is disclosed.

Kinetics of protective efficacy of different mycobacterial preparations



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TB vaccine and diagnostic based on antigens from the *M. tuberculosis* cell

BACKGROUND OF THE INVENTION

Human tuberculosis (TB) caused by *Mycobacterium tuberculosis* is a serious global health problem responsible for approximately 3 million deaths annually, according to WHO. The world-wide incidence of new tuberculosis cases has been progressively falling for the last decade but the recent years have markedly changed this trend due to the advent of AIDS and the appearance of multidrug resistant strains of *Mycobacterium tuberculosis*.

- 10 The only vaccine presently available for clinical use is BCG, a vaccine whose efficacy remains a matter of controversy. BCG generally induces a high level of acquired resistance in animal models of tuberculosis, but several human trials in developing countries have failed to demonstrate significant protection. Notably, BCG is not approved by the FDA for use in the United States because BCG vaccination impairs the specificity of the Tuberculin skin test for diagnosis of TB infection.

- This makes the development of a new and improved vaccine against tuberculosis an urgent matter which has been given a very high priority by the WHO. Many attempts have been made to define the protective Mycobacterial substances and a series of experiments were conducted to compare the protective efficacy of vaccination with live versus killed preparations of *M.tuberculosis* (Orme IM. Infect.Immun.1988; 56:3310-12). The conclusion of these studies was that vaccination of mice with dead *M.tuberculosis* administered without adjuvants only induced short term protection against TB, whereas live *M.tuberculosis* vaccines induced efficient immunological memory. This information was the background for the further search for protective substances focused on antigens actively secreted from the live *Mycobacteria* (Andersen P. Infect.Immun.1994; 62:2536-44, Horwitz et al. Proc. Natl Acad. Sci. USA 1995; 92:1530-4, Pal PG et al. Infect.Immun. 1992; 60: 4781-92).

30 DETAILED DISCLOSURE OF THE INVENTION

The present inventors conducted a study comparing the long term protection against TB after vaccination three times with killed *M.tuberculosis* administered with DDA as an adjuvant with the long term protection obtained with ST-CF, and surprisingly similar levels

of long term protection induced in the group receiving killed bacteria were found as in the group vaccinated with ST-CF/DDA (figure 1).

This leads to the conclusion that protective components can be found also among the
5 components of the cell wall, cell membrane or cytosol derived from a preparation of dead virulent *Mycobacteria*.

It is thus an object of the present invention to provide a composition for the generation or determination of an immune response against a virulent *Mycobacterium* such as a
10 vaccine for immunising a mammal, including a human being, against disease caused by a virulent *Mycobacterium* and a diagnostic reagent for the diagnosis of an infection with a virulent *Mycobacterium*.

By the terms "somatic protein" or "protein derived from the cell wall, the cell membrane or
15 the cytosol", or by the abbreviation "SPE" is understood a polypeptide or a protein extract obtainable from a cell or a part. A preferred method to obtain a somatic protein is described in the examples, especially examples 2, 3, 4, and 5.

By the term "virulent *Mycobacterium*" is understood a bacterium capable of causing the
20 tuberculosis disease in a mammal including a human being. Examples of virulent *Mycobacteria* are *M. tuberculosis*, *M. africanum*, and *M. bovis*.

By "a TB patient" is understood an individual with culture or microscopically proven infection with virulent *Mycobacteria*, and/or an individual clinically diagnosed with TB and
25 who is responsive to anti-TB chemotherapy. Culture, microscopy and clinical diagnosis of TB is well known by the person skilled in the art.

A significant decrease or increase is defined as a decrease or increase which is significant at the 95% level by comparison of immunised and placebo-treated groups
30 using an appropriate statistical analysis such as a Student's two-tailed T test.

By the term "PPD positive individual" is understood an individual with a positive Mantoux test or an individual where PPD induces an increase in *in vitro* recall response determined by release of IFN- γ of at least 1,000 pg/ml from Peripheral Blood
35 Mononuclear Cells (PBMC) or whole blood, the induction being performed by the addition

of 2.5 to 5 µg PPD/ml to a suspension comprising about 1.0 to 2.5 x 10⁵ PBMC, the release of IFN-γ being assessable by determination of IFN-γ in supernatant harvested 5 days after the addition of PPD to the suspension compared to the release of IFN-γ without the addition of PPD.

5

By the term "delayed type hypersensitivity reaction" is understood a T-cell mediated inflammatory response elicited after the injection of a polypeptide into or application to the skin, said inflammatory response appearing 72-96 hours after the polypeptide injection or application.

10

By the term "IFN-γ" is understood interferon-gamma.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations thereof such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

By the term "a polypeptide" in the present application is generally understood a polypeptide of the invention, as will be described later. It is also within the meaning of "a polypeptide" that several polypeptides can be used, i.e. in the present context "a" means "at least one" unless explicitly indicated otherwise. The "polypeptide" is used to refer to short peptides with a length of at least two amino acid residues and at most 10 amino acid residues, oligopeptides (11-100 amino acid residues), and longer peptides (the usual interpretation of "polypeptide", i.e. more than 100 amino acid residues in length) as well as proteins (the functional entity comprising at least one peptide, oligopeptide, or polypeptide which may be chemically modified by being phosphorylated, glycosylated, by being lipidated, or by comprising prosthetic groups). The definition of polypeptides comprises native forms of peptides/proteins in *Mycobacteria* as well as recombinant proteins or peptides in any type of expression vectors transforming any kind of host, and also chemically synthesised polypeptides. Within the scope of the invention is a polypeptide which is at least 6 amino acids long, preferably 7, such as 8, 9, 10, 11, 12, 13, 14 amino acids long, preferably at least 15 amino acids, such as 15, 16, 17, 18, 19, 20 amino acids long. However, also longer polypeptides having a length of e.g. 25, 50, 75, 100, 125, 150, 175 or 200 amino acids are within the scope of the present invention.

35

In the present context the term "purified polypeptide" means a polypeptide preparation which contains at most 5% by weight of other polypeptide material with which it is natively associated (lower percentages of other polypeptide material are preferred, e.g. at most 4%, at most 3%, at most 2%, at most 1%, and at most ½%). It is preferred that the

5 substantially pure polypeptide is at least 96% pure, *i.e.* that the polypeptide constitutes at least 96% by weight of total polypeptide material present in the preparation, and higher percentages are preferred, such as at least 97%, at least 98%, at least 99%, at least 99,25%, at least 99,5%, and at least 99,75%. It is especially preferred that the polypeptide is in "essentially pure form", *i.e.* that the polypeptide is essentially free of any

10 other antigen with which it is natively associated, *i.e.* free of any other antigen from bacteria belonging to the tuberculosis complex. This can be accomplished by preparing the polypeptide by means of recombinant methods in a non-mycobacterial host cell as will be described in detail below, or by synthesising the polypeptide by the well-known methods of solid or liquid phase peptide synthesis, e.g. by the method described by

15 Merrifield or variations thereof.

By the term "non-naturally occurring polypeptide" is understood a polypeptide that does not occur naturally. This means that the polypeptide is substantially pure, and/or that the polypeptide has been synthesised in the laboratory, and/or that the polypeptide has been

20 produced by means of recombinant technology.

By the terms "analogue" and "subsequence" when used in connection with polypeptides is meant any polypeptide having the same immunological characteristics as the polypeptides of the invention described above with respect to the ability to confer

25 increased resistance to infection with virulent *Mycobacteria*. Thus, included is also a polypeptide from a different source, such as from another bacterium or even from a eukaryotic cell.

The term "sequence identity" indicates a quantitative measure of the degree of homology

30 between two amino acid sequences of equal length or between two nucleotide sequences of equal length. If the two sequences to be compared are not of equal length, they must be aligned to best possible fit. The sequence identity can be calculated as

$$\frac{(N_{ref} - N_{dif})100}{N_{ref}}$$

wherein N_{dif} is the total number of non-identical residues in the two sequences when aligned and wherein N_{ref} is the number of residues in one of the sequences. Hence,

35 the DNA sequence AGTCAGTC will have a sequence identity of 75% with the sequence

AATCAATC ($N_{\text{dif}}=2$ and $N_{\text{ref}}=8$). A gap is counted as non-identity of the specific residue(s), i.e. the DNA sequence AGTGTC will have a sequence identity of 75% with the DNA sequence AGTCAGTC ($N_{\text{dif}}=2$ and $N_{\text{ref}}=8$). Sequence identity can alternatively be calculated by the BLAST program e.g. the BLASTP program or the BLASTN program

5 (Pearson W.R and D.J. Lipman (1988) PNAS USA 85:2444-2448)(www.ncbi.nlm.nih.gov/BLAST). In one aspect of the invention, alignment is performed with the global align algorithm with default parameters as described by X. Huang and W. Miller. Adv. Appl. Math. (1991) 12:337-357, available at http://www.ch.embnet.org/software/LALIGN_form.html.

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When the term nucleotide is used in the following, it should be understood in the broadest sense. That is, most often the nucleotide should be considered as DNA. However, when DNA can be substituted with RNA, the term nucleotide should be read to include RNA embodiments which will be apparent for the person skilled in the art. For the purposes of

15 hybridisation, PNA or LNA may be used instead of DNA. PNA has been shown to exhibit a very dynamic hybridisation profile and is described in Nielsen P E *et al.*, 1991, Science 254: 1497-1500). LNA (Locked Nucleic Acids) is a recently introduced oligonucleotide analogue containing bicyclo nucleoside monomers (Koshkin *et al.*, 1998, 54, 3607-3630; Nielsen, N.K. *et al.* J.Am.Chem.Soc 1998, 120, 5458-5463).

20

It is surprisingly demonstrated herein that the SPE comprising polypeptides isolated from the cell wall, cell membrane and cytosol induces protective immunity against infection with *M.tuberculosis* in an animal model, when injected with an adjuvant. It is contemplated that these polypeptides, either alone or in combination, can be used as

25 vaccine components.

It is further demonstrated that several polypeptides isolated from the cell wall, cell membrane or cytosol are recognised by human tuberculosis antisera. Therefore it is considered likely that these polypeptides, either alone or in combination, can be useful as

30 diagnostic reagents in the diagnosis of tuberculosis.

One embodiment of the invention relates to a method for producing a polypeptide in an immunological composition comprising the steps of:

a) killing a sample of virulent *Mycobacteria*;

35 b) centrifugating the sample of a);

- c) resuspending the pellet of b) in PBS;
- d) centrifugating the suspension of c);
- e) extracting soluble proteins from the cytosol as well as cell wall and cell membrane from the supernatant of d) with SDS;
- 5 f) centrifugating the extract of e);
- g) precipitating the supernatant of f) in cold acetone;
- h) resuspending the precipitate of g) in PBS;
- i) applying the resuspension of h) to 2 dimensional electrophoresis;
- j) blotting the gel of i) to a PVDF membrane;
- 10 k) subjecting the spots on j) to N-terminal sequencing;
- l) searching a database for homology with the sequence of k) to identify the nucleotide sequence;
- m) cloning the nucleotide sequence of l) into an expression system;
- n) isolating and purifying the polypeptide expressed in m); and
- 15 o) formulating the polypeptide of n) with an adjuvant substance in an immunological composition.

Another embodiment is a method of producing a polypeptide originating from the cell wall in an immunological composition, said method comprising the steps of:

- 20 a) killing a sample of virulent *Mycobacteria*;
- b) centrifugating the sample of a)
- c) resuspending the pellet of b) in PBS supplemented with EDTA and phenylmethylsulfonyl fluoride and sonicating for 15 min
- d) lysing the suspension of c)
- 25 e) centrifugating the lysed suspension of d)
- f) resuspending the pellet of e) in homogenising buffer
- g) incubating the suspension of f) with RNase and DNase overnight
- h) incubating the suspension of g) with SDS
- i) centrifugating the incubated suspension of h).
- 30 j) incubating the supernatant of i) with SDS
- k) precipitating the incubated supernatant of j) with acetone
- l) resuspending the precipitate of k) in PBS
- m) subjecting the suspension of l) to a Triton X-114 extraction
- n) applying the resuspension of m) to 2 dimensional electrophoresis;
- 35 o) blotting the gel of n) to a PVDF membrane;

- p) subjecting the spots on o) to N-terminal sequencing;
- q) searching a database for homology with the sequence of p) to identify the nucleotide sequence;
- r) cloning the nucleotide sequence of q) into an expression system;
- 5 s) isolating and purifying the polypeptide expressed in r); and
- t) formulating the polypeptide of s) with an adjuvant substance in an immunological composition.

- A third embodiment is a method of producing a polypeptide originating from the cell
- 10 membrane in an immunological composition, said method comprising the steps of:
 - a) killing a sample of virulent *Mycobacteria*;
 - b) centrifugating the sample of a)
 - c) resuspending the pellet of b) in PBS supplemented with EDTA and phenylmethylsulfonyl fluoride and sonicating for 15 min
 - 15 d) lysing the suspension of c)
 - e) centrifugating the lysed suspension of d)
 - f) ultracentrifugating the supernatant of e)
 - g) resuspending the pellet of f) in PBS
 - h) subject the suspension of g) to a Triton X-114 extraction
 - 20 i) applying the resuspension of h) to 2 dimensional electrophoresis;
 - j) blotting the gel of i) to a PVDF membrane;
 - k) subjecting the spots on j) to N-terminal sequencing;
 - l) searching a database for homology with the sequence of k) to identify the nucleotide sequence;
 - 25 m) cloning the nucleotide sequence of l) into an expression system; and
 - n) isolating and purifying the polypeptide expressed in m);
 - o) formulating the polypeptide of n) with an adjuvant substance in an immunological composition.

- 30 A fourth embodiment is a method of producing a polypeptide originating from the cytosol in an immunological composition comprising the steps of:
- a) killing a sample of virulent *Mycobacteria*;
 - b) centrifugating the sample of a)
 - c) resuspending the pellet of b) in PBS supplemented with EDTA and
 - 35 phenylmethylsulfonyl fluoride and sonicating for 15 min

- d) lysing the suspension of c)
- e) centrifugating the lysed suspension of d)
- f) ultracentrifugating the supernatant of e)
- g) precipitating the supernatant of f) with acetone
- 5 h) resuspending the precipitate of g) in PBS
- i) applying the resuspension of h) to 2 dimensional electrophoresis;
- j) plotting the gel of i) to a PVDF membrane;
- k) subjecting the spots on j) to N-terminal sequencing;
- l) searching a database for homology with the sequence of k) to identify the nucleotide
- 10 sequence;
- m) cloning the nucleotide sequence of l) into an expression system;
- n) isolating and purifying the polypeptide expressed in m); and
- o) formulating the polypeptide of n) with an adjuvant substance in an immunological composition.

15

In particular, the invention relates to a polypeptide obtainable by a method as described above which polypeptide has at least one of the following properties:

- i) it induces an *in vitro* recall response determined by a release of IFN- γ of at least 1,500
- 20 pg/ml from reactivated memory T-lymphocytes withdrawn from a C57Bl/6J mouse within 4 days after the mouse has been rechallenged with 1×10^6 virulent *Mycobacteria*, the induction being performed by the addition of the polypeptide to a suspension comprising about 2×10^5 cells isolated from the spleen of said mouse, the addition of the polypeptide resulting in a concentration of the polypeptide of not more than 20 μ g per ml suspension,
- 25 the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 3 days after the addition of the polypeptide to the suspension,
- ii) it induces an *in vitro* response during primary infection with virulent *Mycobacteria*, determined by release of IFN- γ of at least 1,500 pg/ml from T-lymphocytes withdrawn
- 30 from a mouse within 28 days after the mouse has been infected with 5×10^4 virulent *Mycobacteria*, the induction being performed by the addition of the polypeptide to a suspension comprising about 2×10^5 cells isolated from the spleen, the addition of the polypeptide resulting in a concentration of not more than 20 μ g per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 3
- 35 days after the addition of the polypeptide to the suspension,

- iii) it induces a protective immunity determined by vaccinating an animal model with the polypeptide and an adjuvant in a total of three times with two weeks interval starting at 6-8 weeks of age, 6 weeks after the last vaccination challenging with 5×10^6 virulent *Mycobacterium*/ml by aerosol and determining a significant decrease in the number of bacteria recoverable from the lung 6 weeks after the animal has been challenged, compared to the number recovered from the same organ in a mammal given placebo treatment,
- iv) it induces *in vitro* recall response determined by release of IFN- γ of at least 1,000 pg/ml from Peripheral Blood Mononuclear Cells (PBMC) or whole blood withdrawn from TB patients 0-6 months after diagnosis, or PPD positive individual, the induction being performed by the addition of the polypeptide to a suspension comprising about 1.0 to 2.5×10^5 PBMC or whole blood cells, the addition of the polypeptide resulting in a concentration of not more than 20 μ g per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 5 days after the addition of the polypeptide to the suspension,
- v) it induces a specific antibody response in a TB patient as determined by an ELISA technique or a western blot when the whole blood is diluted 1:20 in PBS and stimulated with the polypeptide in a concentration of at the most 20 μ g/ml and induces an OD of at least 0.1 in ELISA, or a visual response in western blot.
- vi) it induces a positive *in vitro* response determined by release of IFN- γ of at least 500 pg/ml from Peripheral Blood Mononuclear Cells (PBMC) withdrawn from an individual who is clinically or subclinically infected with a virulent *Mycobacterium*, the induction being performed by the addition of the polypeptide to a suspension comprising about 1.0 to 2.5×10^5 PBMC, the addition of the polypeptide resulting in a concentration of not more than 20 μ g per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 5 days after the addition of the polypeptide to the suspension, and preferably does not induce such an IFN- γ release in an individual not infected with a virulent *Mycobacterium*,
- vii) it induces a positive *in vitro* response determined by release of IFN- γ of at least 500 pg/ml from Peripheral Blood Mononuclear Cells (PBMC) withdrawn from an individual

clinically or subclinically infected with a virulent *Mycobacterium*, the induction being performed by the addition of the polypeptide to a suspension comprising about 1.0 to 2.5×10^5 PBMC, the addition of the polypeptide resulting in a concentration of not more than $20 \mu\text{g}$ per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 5 days after the addition of the polypeptide to the suspension, and preferably does not induce such an IFN- γ release in an individual not infected with a virulent *Mycobacterium*,

viii) it induces a positive DTH response determined by intradermal injection or local application patch of at most $100 \mu\text{g}$ of the polypeptide to an individual who is clinically or subclinically infected with a virulent *Mycobacterium*, a positive response having a diameter of at least 10 mm 72-96 hours after the injection or application,

ix) it induces a positive DTH response determined by intradermal injection or local application patch of at most $100 \mu\text{g}$ of the polypeptide to an individual who is clinically or subclinically infected with a virulent *Mycobacterium*, a positive response having a diameter of at least 10 mm 72-96 hours after the injection, and preferably does not induce a such response in an individual who has a cleared infection with a virulent *Mycobacterium*.

20

Any polypeptide fulfilling one or more of the above properties and which is obtainable from either the cell wall, cell membrane or the cytosol is within the scope of the present invention.

25 The property described in i) will also be satisfied if the release of IFN- γ from reactivated memory T-lymphocytes is $2,000 \text{ pg/ml}$, such as $3,000 \text{ pg/ml}$. In an alternative embodiment of the invention, the immunological effect of the polypeptide could be determined by comparing the IFN- γ release as described with the IFN- γ release from a similar assay, wherein the polypeptide is not added, a significant increase being
30 indicative of an immunologically effective polypeptide. In a preferred embodiment of the invention, the addition of the polypeptide results in a concentration of not more than $20 \mu\text{g}$ per ml suspension, such as $15 \mu\text{g}$, $10 \mu\text{g}$, $5 \mu\text{g}$, $3 \mu\text{g}$, $2 \mu\text{g}$, or $1 \mu\text{g}$ polypeptide per ml suspension.

The property mentions as an example the mouse strain C57Bl/6j as the animal model. As will be known by a person skilled in the art, due to genetic variation, different strains may react with immune responses of varying strength to the same polypeptide. It is presently unknown which strains of mice will give the best predictability of immunogenic reactivity
5 in which human population. Therefore, it is important to test other mouse strains, such as C3H/HeN, CBA (preferably CBA/J), DBA (preferably DBA/2J), A/J, AKR/N, DBA/1J, FVB/N, SJL/N, 129/SvJ, C3H/HeJ-*Lps* or BALB mice (preferably BALB/cA, BALB/cJ). It is presently contemplated that also a similar test performed in another animal model such as a guinea pig or a rat will have clinical predictability. In order to obtain good clinical
10 predictability to humans, it is contemplated that any farm animal, such as a cow, pig, or deer, or any primate will have clinical predictability and thus serve as an animal model.

It should be noted, moreover, that tuberculosis disease also affects a number of different animal species such as cows, primates, guinea pigs, badgers, possums, and deers. A
15 polypeptide which has proven effective in any of the models mentioned above may be of interest for animal treatment even if it is not effective in a human being.

It is proposed to measure the release of IFN- γ from reactivated T lymphocytes withdrawn from a C57Bl/6j mouse within 4 days after the mouse has been rechallenged with virulent
20 *Mycobacteria*. This is due to the fact that when an immune host mounts a protective immune response, the specific T-cells responsible for the early recognition of the infected macrophage stimulate a powerful bactericidal activity through their production of IFN- γ (Rook, G.A.W. (1990) Res. Microbiol. 141:253-256; Flesch, I. et S.H.E. Kaufmann (1987) J Immunol. 138(12):4408-13). However other cytokines could be relevant when
25 monitoring the immunological response to the polypeptide, such as IL-12, TNF- α , IL-4, IL-5, IL-10, IL-6, TGF- β . Usually one or more cytokines will be measured utilising for example the PCR technique or ELISA. It will be appreciated by the person skilled in the art that a significant increase or decrease in the amount of any of these cytokines induced by a specific polypeptide can be used in evaluation of the immunological efficacy
30 of the polypeptide. The ability of a polypeptide to induce a IFN- γ response is presently believed to be the most relevant correlate of protective immunity as mice with a disruption of the gene coding for IFN- γ are unable to control a mycobacterial infection and die very rapidly with widespread dissemination, caseous necrosis and large abscesses (Flynn et al (1993) J.Exp.Med 178: 2249-2254, Cooper et al (1993) J.Exp.Med. 178:2243-2248). A
35 specific model for obtaining information regarding the antigenic targets of a protective

immunity in the memory model was originally developed by Lefford (Lefford et al (1973) Immunology 25:703) and has been used extensively in the recent years (Orme et al (1988). Infect.Immun. 140:3589, P.Andersen and I. Heron (1993) J.Immunol.154:3359).

- 5 The property described in ii) will also be satisfied if the release of IFN- γ from T-lymphocytes withdrawn during primary infection is 2,000 pg/ml, such as 3,000 pg/ml. The comments on property i) regarding a significant increase in IFN- γ , concentration of polypeptide, animal model, and other cytokines are equally relevant to property ii), and *vice versa*.

10

- The property described in iii) will also be satisfied if the protective immunity is determined by challenging the mouse more than 6 weeks after the last vaccination challenge such as 7 weeks, preferably 8 weeks, 9 weeks, 10 weeks, 11 weeks, 12 weeks or 15 weeks. In one embodiment of the invention the bacteria are recovered from the spleen more than 6 weeks after the last vaccination challenge such as 7 weeks, preferably 8 weeks, 9 weeks, 10 weeks, 11 weeks, 12 weeks or 15 weeks. In another embodiment of the invention, the last vaccination challenge is given subcutaneously with 5×10^4 virulent *Mycobacteria*. As will be known by the person skilled in the art, the number of viable bacteria in the lung is presently considered to be relevant to the degree of bacterial infection of the animal. An equally important measure is the determination of the number of viable bacteria in the spleen, lymph node, or blood.

- The amount of polypeptide and adjuvant used for vaccinating will depend on the animal model used, e.g. the mouse strain. When a mouse model is used it is preferred that the amount of polypeptide used for vaccinating the mouse is between 2 and 20 μg , such as between 5 and 15 μg , preferably 10 μg . For larger animals such as guinea pigs, deers, cows, primates, badgers, and possums higher doses such as 5 to 50 μg of a single polypeptide are preferred.

- 30 The comments on property i) regarding concentration of polypeptide and animal model are equally relevant to property iii), and *vice versa*.

- In another aspect of property iii), the mice, or other animal model, are given the standard lethal dose of virulent *Mycobacteria*. The standard lethal dose varies from around 3×10^5 to around 5×10^6 virulent *Mycobacteria* depending on the specific strain of virulent

Mycobacteria and strain of mice. The mortality in the mice is then monitored and compared to a placebo vaccinated control group. A significant decrease in mortality, measured as the mean survival time, will be indicative of an immunologically effective polypeptide. In a very recent paper it is shown that there is good correlation between

5 mortality of the individual animals and the bacterial counts in the same animals.

(S.Baldwin (1998) Infect.Immun 66:2951-2959).

The property described in iv) will also be satisfied if the release of IFN- γ from PBMC is determined in PBMC withdrawn from TB patients or PPD positive individuals more than 6
10 months after diagnosis such as 9 months, 1 year, 2 years, 5 years, or 10 years after diagnosis.

The comments on property i) regarding significant increase in IFN- γ , concentration of polypeptide, and other cytokines are equally relevant to property iv).

15

The property described in v) will in particular be satisfied, if the ELISA is performed as follows: the polypeptide of interest in the concentration of 1 to 10 $\mu\text{g/ml}$ is coated on a 96 wells polystyrene plate (NUNC, Denmark) and after a washing step with phosphate buffer pH 7.3, containing 0.37 M NaCl and 0.5% Tween-20 the serum or plasma from a TB
20 patient is applied in dilution's from 1:10 to 1:1000 in PBS with 1% Tween-20. Binding of an antibody to the polypeptide is determined by addition of a labeled (e.g. peroxidase labeled) secondary antibody and reaction is thereafter visualized by the use of OPD and H_2O_2 as described by the manufacturer (DAKO, Denmark). The OD value in each well is determined using an appropriate ELISA reader.

25

In a preferred embodiment the western blot is performed as follows: The polypeptide is applied in concentrations from 1-40 μg to a SDS-PAGE and after electrophoresis the polypeptide is transferred to a membrane e.g. nitrocellulose or PVDF. The membrane is thereafter washed in phosphate buffer, pH 7.3, containing 0.37 M NaCl and 0.5% Tween-
30 20 for 30 min. The sera obtained from one or more TB patients were diluted 1:10 to 1:1000 in phosphate buffer pH 7.3 containing 0.37 M NaCl. The membrane is hereafter washed four times five minutes in binding buffer and incubated with peroxidase- or phosphates-labeled secondary antibody. Reaction is then visualized using the staining method recommended by the manufacture (DAKO, Denmark).

35

The property described in vi) will in particular be satisfied if the polypeptide does not induce such an IFN- γ release in an individual not infected with a virulent *Mycobacterium*, i.e. an individual who has been BCG vaccinated or infected with *Mycobacterium avium* or sensitised by non-tuberculosis *Mycobacterium* (NTM). The comments on property i) regarding significant increase in IFN- γ , concentration of polypeptide, and other cytokines are equally relevant to property vi).

The property described in vii) will in particular be satisfied if the polypeptide does not induce such an IFN- γ release in an individual cleared of an infection with a virulent *Mycobacterium*, i.e. which does not have any positive culture, microscopically or clinically proven ongoing infection with virulent *Mycobacterium*. The comments on property i) regarding significant increase in IFN- γ , concentration of polypeptide, and other cytokines are equally relevant to property vii).

The property described in viii) will in particular be satisfied if the polypeptide does not induce such a response in an individual not infected with a virulent *Mycobacterium*, i.e. an individual who has been BCG vaccinated or infected with *Mycobacterium avium* or sensitised by non-tuberculosis *Mycobacterium*. In a preferred embodiment the amount of polypeptide intradermally injected or applied is 90 μ g, such as 80 μ g, 70 μ g, 60 μ g, 50 μ g, 40 μ g, or 30 μ g. In another embodiment of the invention, the diameter of the positive response is at least 11 mm, such as 12 mm, 13 mm, 14 mm, or 15 mm. In a preferred embodiment the induration of erythema or both could be determined after administration of the polypeptide by intradermal injection, patch test or multipuncture. The reaction diameter could be positive after more than 48, such as 72 or 96 hours.

25

The property described in ix) will in particular be satisfied if the polypeptide does not induce such a response in an individual cleared of an infection with a virulent *Mycobacterium*, i.e. which does not have any positive culture or microscopically proven ongoing infection with virulent *Mycobacterium*. The comments on property viii) regarding the amount of polypeptide intradermally injected or applied and the diameter of the positive response are equally relevant to property ix).

Preferred embodiments of the invention are the specific polypeptides which have been identified and analogues and subsequences thereof. It has been noted that none of the identified polypeptides in the examples include a signal sequence.

Until the present invention was made, it was unknown that the polypeptides with the amino acid sequences disclosed in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 75, 77 and 79 are expressed in live virulent *Mycobacterium*.

5 These polypeptides in purified form, or non-naturally occurring, i.e. recombinantly or synthetically produced, are considered part of the invention. It is understood that a polypeptide which has any of the properties i) - ix) and has a sequence identity of at least 80% with any of the amino acid sequences shown in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 75, 77 and 79 or has a sequence identity of
10 at least 80% to any subsequence thereof is considered part of the invention. In a preferred embodiment the sequence identity is at least 80%, such as 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.5%. Furthermore, any T cell epitope of the polypeptides disclosed in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 75, 77 and 79 is
15 considered part of the invention. Also, any B-cell epitope of the polypeptides disclosed in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 75, 77 and 79 is considered part of the invention.

Although the minimum length of a T-cell epitope has been shown to be at least 6 amino
20 acids, it is normal that such epitopes are constituted of longer stretches of amino acids. Hence it is preferred that the polypeptide fragment of the invention has a length of at least 7 amino acid residues, such as at least 8, at least 9, at least 10, at least 12, at least 14, at least 16, at least 18, at least 20, at least 22, at least 24, or at least 30 amino acid residues.

25

In both immunodiagnostics and vaccine preparation, it is often possible and practical to prepare antigens from segments of a known immunogenic protein or polypeptide. Certain epitopic regions may be used to produce responses similar to those produced by the entire antigenic polypeptide. Potential antigenic or immunogenic regions may be
30 identified by any of a number of approaches, e.g., Jameson-Wolf or Kyte-Doolittle antigenicity analyses or Hopp and Woods (Hopp et Woods, (1981), Proc Natl Acad Sci USA 78/6:3824-8) hydrophobicity analysis (see, e.g., Jameson and Wolf, (1988) Comput Appl Biosci, 4(1):181-6; Kyte and Doolittle, (1982) J Mol Biol, 157(1):105-32; or U.S. Patent No. 4,554,101). Hydrophobicity analysis assigns average hydrophilicity values to
35 each amino acid residue; from these values average hydrophilicities can be calculated

and regions of greatest hydrophilicity determined. Using one or more of these methods, regions of predicted antigenicity may be derived from the amino acid sequence assigned to the polypeptides of the invention. Alternatively, in order to identify relevant T-cell epitopes which are recognised during an immune response, it is also possible to use a "brute force" method: Since T-cell epitopes are linear, deletion mutants of polypeptides will, if constructed systematically, reveal what regions of the polypeptide are essential in immune recognition, e.g. by subjecting these deletion mutants to the IFN- γ assay described herein. A presently preferred method utilises overlapping oligomers (preferably synthetic ones having a length of e.g. 20 amino acid residues) derived from the polypeptide. Some of these will give a positive response in the IFN- γ assay whereas others will not. A preferred T-cell epitope is a T-helper cell epitope or a cytotoxic T-cell epitope.

B-cell epitopes may be linear or spatial. The three-dimensional structure of a protein is often such that amino acids, which are located distant from each other in the one-dimensional structure, are located near to each other in the folded protein. Within the meaning of the present context, the expression epitope is intended to comprise the one- and three-dimensional structure as well as mimics thereof. The term is further intended to include discontinuous B-cell epitopes. The linear B-cell epitopes can be identified in a similar manner as described for the T-cell epitopes above. However, when identifying B-cell epitopes the assay should be an ELISA using overlapping oligomers derived from the polypeptide as the coating layer on a microtiter plate as described elsewhere.

A non-naturally occurring polypeptide, an analogue, a subsequence, a T-cell epitope and/or a B-cell epitope of any of the described polypeptides are defined as any non-naturally occurring polypeptide, analogue, subsequence, T-cell epitope and/or B-cell epitope of any of the polypeptides having any of the properties i)-ix).

Table 1 lists the antigens of the invention.

Table 1 The antigens of the invention by the names used herein as well as by reference to relevant SEQ ID NOs of N-terminal sequences, full amino acid sequences and sequences of nucleotides encoding the antigens

Antigen	N-Terminal sequence SEQ ID NO:	Nucleotide sequence SEQ ID NO:	Amino acid sequence SEQ ID NO:
TB10C	45	1	2
TB13A	50	3	4
TB15	39	5	6
TB15A	46	7	8
TB17	47	9	10
TB18	40	11	12
TB21	41	13	14
TB24	48	15	16
TB27B	49	17	18
TB33	42	19	20
TB38	43	21	22
TB54	44	23	24
TB64	57	25	26
TB11B	51	27	28
TB16	52	29	30
TB16A	53	31	32
TB32	54	33	34
TB32A	55	35	36
TB51	56	37	38
TB12.5	80	74	75
TB20.6	81	76	77
TB40.8	82	78	79

- 5 Each of the polypeptides may be characterised by specific amino acid and nucleic acid sequences. It will be understood that such sequences include analogues and variants produced by recombinant methods wherein such nucleic acid and polypeptide sequences have been modified by substitution, insertion, addition and/or deletion of one or more nucleotides in said nucleic acid sequences to cause the substitution, insertion, addition or
- 10 deletion of one or more amino acid residues in the recombinant polypeptide. A preferred nucleotide sequence encoding a polypeptide of the invention is a nucleotide sequence which

- 1) is a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 74, 76 and 78 or an analogue of said sequence which hybridises with any of the nucleotide sequences shown in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 74, 76 or 78 or a
5 nucleotide sequence complementary thereto, or a specific part thereof, preferably under stringent hybridisation conditions. By stringent conditions is understood, as defined in the art, 5-10°C under the melting point T_m , cf. Sambrook et al, 1989, pages 11.45-11.49, and/or
- 10 2) encodes a polypeptide, the amino acid sequence of which has a 80% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 75, 77 and 79 and/or
- 3) constitutes a subsequence of any of the above mentioned nucleotide sequences,
15 and/or
- 4) constitutes a subsequence of any of the above mentioned polypeptide sequences.

The terms "analogue" or "subsequence" when used in connection with the nucleotide
20 fragments of the invention are thus intended to indicate a nucleotide sequence which encodes a polypeptide exhibiting identical or substantially identical immunological properties to a polypeptide encoded by the nucleotide fragment of the invention shown in any of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 74, 76 or 78, allowing for minor variations which do not have an adverse effect on the ligand
25 binding properties and/or biological function and/or immunogenicity as compared to any of the polypeptides of the invention or which give interesting and useful novel binding properties or biological functions and immunogenicities etc. of the analogue and/or subsequence. The analogous nucleotide fragment or nucleotide sequence may be derived from a bacterium, a mammal, or a human or may be partially or completely of
30 synthetic origin. The analogue and/or subsequence may also be derived through the use of recombinant nucleotide techniques.

Furthermore, the terms "analogue" and "subsequence" are intended to allow for variations in the sequence such as substitution, insertion (including introns), addition,
35 deletion and rearrangement of one or more nucleotides, which variations do not have any

substantial effect on the polypeptide encoded by a nucleotide fragment or a subsequence thereof. The term "substitution" is intended to mean the replacement of one or more nucleotides in the full nucleotide sequence with one or more different nucleotides, "addition" is understood to mean the addition of one or more nucleotides at either end of
5 the full nucleotide sequence, "insertion" is intended to mean the introduction of one or more nucleotides within the full nucleotide sequence, "deletion" is intended to indicate that one or more nucleotides have been deleted from the full nucleotide sequence whether at either end of the sequence or at any suitable point within it, and "re-arrangement" is intended to mean that two or more nucleotide residues have been
10 exchanged with each other.

It is well known that the same amino acid may be encoded by various codons, the codon usage being related, *inter alia*, to the preference of the organisms in question expressing the nucleotide sequence. Thus, at least one nucleotide or codon of a nucleotide fragment
15 of the invention may be exchanged by others which, when expressed, results in a polypeptide identical or substantially identical to the polypeptide encoded by the nucleotide fragment in question.

The term "subsequence" when used in connection with the nucleic acid fragments of the
20 invention is intended to indicate a continuous stretch of at least 10 nucleotides which exhibits the above hybridization pattern. Normally this will require a minimum sequence identity of at least 70% with a subsequence of the hybridization partner having SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 74, 76 or 78. It is preferred that the nucleic acid fragment is longer than 10 nucleotides, such as at least 15,
25 at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, and at least 80 nucleotides long, and the sequence identity should preferable also be higher than 70%, such as at least 75%, at least 80%, at least 85%, at least 90%, at least 92%, at least 94%, at least 96%, and at least 98%. It is most preferred that the sequence identity is 100%. Such fragments may
30 be readily prepared by, for example, directly synthesizing the fragment by chemical means, by application of nucleic acid reproduction technology, such as the PCR technology of U.S. Patent 4,603,102, or by introducing selected sequences into recombinant vectors for recombinant production.

The nucleotide sequence to be modified may be of cDNA or genomic origin as discussed above, but may also be of synthetic origin. Furthermore, the sequence may be of mixed cDNA and genomic, mixed cDNA and synthetic or genomic and synthetic origin as discussed above. The sequence may have been modified, e.g. by site-directed mutagenesis, to result in the desired nucleic acid fragment encoding the desired polypeptide.

The invention also relates to a replicable expression vector which comprises a nucleic acid fragment defined above, especially a vector which comprises a nucleic acid fragment encoding a polypeptide fragment of the invention. The vector may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, *i.e.* a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication; examples of such a vector are a plasmid, phage, cosmid, mini-chromosome and virus. Alternatively, the vector may be one which, when introduced in a host cell, is integrated in the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

Expression vectors may be constructed to include any of the DNA segments disclosed herein. Such DNA might encode an antigenic protein specific for virulent strains of mycobacteria or even hybridization probes for detecting mycobacteria nucleic acids in samples. Longer or shorter DNA segments could be used, depending on the antigenic protein desired. Epitopic regions of the proteins expressed or encoded by the disclosed DNA could be included as relatively short segments of DNA. A wide variety of expression vectors is possible including, for example, DNA segments encoding reporter gene products useful for identification of heterologous gene products and/or resistance genes such as antibiotic resistance genes which may be useful in identifying transformed cells.

The vector of the invention may be used to transform cells so as to allow propagation of the nucleic acid fragments of the invention or so as to allow expression of the polypeptide fragments of the invention. Hence, the invention also pertains to a transformed cell harbouring at least one such vector according to the invention, said cell being one which does not natively harbour the vector and/or the nucleic acid fragment of the invention contained therein. Such a transformed cell (which is also a part of the invention) may be

any suitable bacterial host cell or any other type of cell such as a unicellular eukaryotic organism, a fungus or yeast, or a cell derived from a multicellular organism, e.g. an animal or a plant. It is especially in cases where glycosylation is desired that a mammalian cell is used, although glycosylation of proteins is a rare event in prokaryotes. Normally,

5 however, a prokaryotic cell is preferred such as a bacterium belonging to the genera *Mycobacterium*, *Salmonella*, *Pseudomonas*, *Bacillus* and *Eschericia*. It is preferred that the transformed cell is an *E. coli*, *B. subtilis*, or *M. bovis* BCG cell, and it is especially preferred that the transformed cell expresses a polypeptide according of the invention.

The latter opens for the possibility to produce the polypeptide of the invention by simply
10 recovering it from the culture containing the transformed cell. In the most preferred embodiment of this part of the invention the transformed cell is *Mycobacterium bovis* BCG strain: Danish 1331, which is the *Mycobacterium bovis* strain Copenhagen from the Copenhagen BCG Laboratory, Statens Seruminstitut, Denmark.

15 The nucleic acid fragments of the invention allow for the recombinant production of the polypeptides fragments of the invention. However, also isolation from the natural source is a way of providing the polypeptide fragments as is peptide synthesis.

Therefore, the invention also pertains to a method for the preparation of a polypeptide
20 fragment of the invention, said method comprising inserting a nucleic acid fragment as described in the present application into a vector which is able to replicate in a host cell, introducing the resulting recombinant vector into the host cell (transformed cells may be selected using various techniques, including screening by differential hybridization, identification of fused reporter gene products, resistance markers, anti-antigen antibodies
25 and the like), culturing the host cell in a culture medium under conditions sufficient to effect expression of the polypeptide (of course the cell may be cultivated under conditions appropriate to the circumstances; and if DNA is desired, replication conditions are used), and recovering the polypeptide from the host cell or culture medium; or

30 isolating the polypeptide from a short-term culture filtrate; or

isolating the polypeptide from whole mycobacteria of the tuberculosis complex or from lysates or fractions thereof, e.g. cell wall containing fractions, or

35 synthesizing the polypeptide by solid or liquid phase peptide synthesis.

The medium used to grow the transformed cells may be any conventional medium suitable for the purpose. A suitable vector may be any of the vectors described above, and an appropriate host cell may be any of the cell types listed above. The methods
5 employed to construct the vector and effect introduction thereof into the host cell may be any methods known for such purposes within the field of recombinant DNA. In the following a more detailed description of the possibilities will be given:

In general, of course, prokaryotes are preferred for the initial cloning of nucleic se-
10 quences of the invention and constructing the vectors useful in the invention. For example, in addition to the particular strains mentioned in the more specific disclosure below, one may mention by way of example, strains such as *E. coli* K12 strain 294 (ATCC No. 31446), *E. coli* B, and *E. coli* X 1776 (ATCC No. 31537). These examples are, of course, intended to be illustrative and not limiting.

15 Prokaryotes are also preferred for expression. The aforementioned strains, as well as *E. coli* W3110 (F-, lambda-, prototrophic, ATCC No. 273325), bacilli such as *Bacillus subtilis*, or other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcesans*, and various *Pseudomonas* species may be used. Especially interesting are
20 rapid-growing mycobacteria, e.g. *M. smegmatis*, as these bacteria have a high degree of resemblance with mycobacteria of the tuberculosis complex and therefore stand a good chance of reducing the need of performing post-translational modifications of the expression product.

25 In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (see, e.g.,
30 Bolivar et al., 1977, Gene 2: 95). The pBR322 plasmid contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR plasmid, or other microbial plasmids or phages must also contain, or be modified to contain, promoters which can be used by the microorganism for expression.

Those promoters most commonly used in recombinant DNA construction include the B-lactamase (penicillinase) and lactose promoter systems (Chang et al., (1978), Nature, 35:515; Itakura et al., (1977), Science 198:1056; Goeddel et al., (1979), Nature 281:544) and a tryptophan (trp) promoter system (Goeddel et al., (1979) Nature 281:544; EPO 5 Appl. Publ. No. 0036776). While these are the most commonly used, other microbial promoters have been discovered and utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally with plasmid vectors (Siebwenlist et al., (1980), Cell, 20:269). Certain genes from prokaryotes may be expressed efficiently in *E. coli* from their own promoter sequences, precluding the 10 need for addition of another promoter by artificial means.

After the recombinant preparation of the polypeptide according to the invention, the isolation of the polypeptide may for instance be carried out by affinity chromatography (or other conventional biochemical procedures based on chromatography), using a 15 monoclonal antibody which substantially specifically binds the polypeptide according to the invention. Another possibility is to employ the simultaneous electroelution technique described by Andersen *et al.* in J. Immunol. Methods **161**: 29-39.

According to the invention the post-translational modifications involves lipidation, gly- 20 cosylation, cleavage, or elongation of the polypeptide.

In certain aspects, the DNA sequence information provided by this invention allows for the preparation of relatively short DNA (or RNA or PNA) sequences having the ability to specifically hybridize to mycobacterial gene sequences. In these aspects, nucleic acid 25 probes of an appropriate length are prepared based on a consideration of the relevant sequence. The ability of such nucleic acid probes to specifically hybridize to the mycobacterial gene sequences lend them particular utility in a variety of embodiments. Most importantly, the probes can be used in a variety of diagnostic assays for detecting the presence of pathogenic organisms in a given sample. However, either uses are 30 envisioned, including the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructs.

Apart from their use as starting points for the synthesis of polypeptides of the invention and for hybridization probes (useful for direct hybridization assays or as primers in e.g. 35 PCR or other molecular amplification methods) the nucleic acid fragments of the

invention may be used for effecting *in vivo* expression of antigens, *i.e.* the nucleic acid fragments may be used in so-called DNA vaccines. Recent research have revealed that a DNA fragment cloned in a vector which is non-replicative in eukaryotic cells may be introduced into an animal (including a human being) by e.g. intramuscular injection or
5 percutaneous administration (the so-called "gene gun" approach). The DNA is taken up by e.g. muscle cells and the gene of interest is expressed by a promoter which is functioning in eukaryotes, e.g. a viral promoter, and the gene product thereafter stimulates the immune system. These newly discovered methods are reviewed in Ulmer et al., (1993), Curr. Opin. Invest. Drugs, 2:983-989 which hereby is included by reference.

10

Hence, the invention also relates to a vaccine comprising a nucleic acid fragment according to the invention, the vaccine effecting *in vivo* expression of antigen by an animal, including a human being, to whom the vaccine has been administered, the amount of expressed antigen being effective to confer substantially increased resistance to infec-
15 tions with mycobacteria of the tuberculosis complex in an animal, including a human being.

The efficacy of such a "DNA vaccine" can possibly be enhanced by administering the gene encoding the expression product together with a DNA fragment encoding a poly-
20 peptide which has the capability of modulating an immune response. For instance, a gene encoding lymphokine precursors or lymphokines (e.g. IFN- γ , IL-2, or IL-12) could be administered together with the gene encoding the immunogenic protein, either by administering two separate DNA fragments or by administering both DNA fragments included in the same vector. It also is a possibility to administer DNA fragments compri-
25 sing a multitude of nucleotide sequences which each encode relevant epitopes of the polypeptides disclosed herein so as to effect a continuous sensitization of the immune system with a broad spectrum of these epitopes.

In one embodiment of the invention, any of the above mentioned polypeptides is used in
30 the manufacture of an immunogenic composition to be used for induction of an immune response in a mammal against an infection with a virulent *Mycobacterium*. Preferably, the immunogenic composition is used as a vaccine.

The preparation of vaccines which contain peptide sequences as active ingredients is
35 generally well understood in the art, as exemplified by U.S. Patents 4,608,251;

4,601,903; 4,599,231; 4,599,230; 4,596,792; and 4,578,770, all incorporated herein by reference. Typically, such vaccines are prepared as injectables either as liquid solutions or suspensions; solid forms suitable for solution in liquid or suspension in liquid prior to injection may also be prepared. The preparation may also be emulsified. The active
5 immunogenic ingredient is often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like, and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants which enhance
10 the effectiveness of the vaccines.

In one embodiment the composition used for vaccination comprises at least one, but preferably at least 2, such as at least 3, 4, 5, 10, 15 or at least 20 different polypeptides of the invention.

15

In another embodiment the composition to be used for vaccine comprises, together with at least one polypeptide of the invention, at least one, but preferably at least 2, such as at least 3, 4, 5, 10, 15 or at least 20 polypeptides which are not polypeptides of the present invention but are derived from a virulent *Mycobacterium* such as a polypeptide belonging
20 to the group of ST-CF (Elhay MJ and Andersen P, Immunology and cell Biology (1997) 75, 595-603). ESAT-6, CFP7, CFP10 (EMBL accession number: AL022120), CFP17, CFP21, CFP25, CFP29, MPB59, MPT59, MPB64, and MPT64.

The vaccines are conventionally administered parenterally, by injection, for example,
25 either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkalene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1-2%. Oral
30 formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10-95% of active ingredient, preferably 25-70%.

35

The proteins may be formulated into the vaccine as neutral or salt forms.

Pharmaceutically acceptable salts include acid addition salts (formed with the free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric,

5 mandelic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

10 The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective and immunogenic. The quantity to be administered depends on the subject to be treated, including, e.g., the capacity of the individual's immune system to mount an immune response, and the degree of protection desired. Suitable dosage ranges are of the order of several hundred micrograms of active
15 ingredient per vaccination with a preferred range from about 0.1 μg to 1000 μg , such as in the range from about 1 μg to 300 μg , and especially in the range from about 10 μg to 50 μg . Suitable regimes for initial administration and booster shots are also variable but are typified by an initial administration followed by subsequent inoculations or other administrations.

20

The manner of application may be varied widely. Any of the conventional methods for administration of a vaccine are applicable. Preferred routes of administration are the parenteral route such as the intravenous, intraperitoneal, intramuscular, subcutaneous or intradermal routes; the oral (on a solid physiologically acceptable base or in a physiologi-
25 cally acceptable dispersion), buccal, sublingual, nasal, rectal or transdermal routes. The dosage of the vaccine will depend on the route of administration and will vary according to the age of the person to be vaccinated and, to a lesser degree, the weight of the person to be vaccinated.

30 Some of the polypeptides of the vaccine are sufficiently immunogenic in a vaccine, but for some of the others the immune response will be enhanced if the vaccine further comprises an adjuvant substance.

Various methods of achieving adjuvant effect for the vaccine include use of agents such
35 as aluminum hydroxide or phosphate (alum), commonly used as a 0.05 to 0.1 percent

solution in phosphate buffered saline, admixture with synthetic polymers of sugars (Carbopol) used as a 0.25 percent solution, aggregation of the protein in the vaccine by heat treatment with temperatures ranging between 70° to 101°C for 30 second to 2 minute periods respectively. Aggregation by reactivating with pepsin treated (Fab) antibodies to albumin, mixture with bacterial cells such as *C. parvum* or endotoxins or lipopolysaccharide components of gram-negative bacteria, emulsion in physiologically acceptable oil vehicles such as mannide mono-oleate (Aracel A) or emulsion with 20 percent solution of a perfluorocarbon (Fluosol-DA) used as a block substitute may also be employed. According to the invention DDA (dimethyldioctadecylammonium bromide) is an interesting candidate for an adjuvant, but also Freund's complete and incomplete adjuvants as well as QuilA and RIBI adjuvants are interesting possibilities.

Other possibilities to enhance the immunogenic effect involve the use of immune modulating substances such as lymphokines (e.g. IFN- γ , IL-2 and IL-12) or synthetic IFN- γ inducers such as poly I:C in combination with the above-mentioned adjuvants.

In many instances, it will be necessary to have multiple administrations of the vaccine, usually not exceeding six vaccinations, more usually not exceeding four vaccinations and preferably one or more, usually at least about three vaccinations. The vaccinations will normally be at from two to twelve week intervals, more usually from three to five week intervals. Periodic boosters at intervals of 1-25 years, such as 20 years, preferably 15 or 10 years, more preferably 1-5 years usually three years, will be desirable to maintain the desired levels of protective immunity.

In one embodiment of the invention a composition is produced comprising as the effective component a micro-organism, the micro-organism is a bacterium such as *Mycobacterium*, *Salmonella*, *Pseudomonas* and *Escherichia*, preferably *Mycobacterium bovis* BCG wherein at least one, such as at least 2 copies, such as at least 5 copies of a nucleotide fragment comprising a nucleotide sequence encoding a polypeptide of the invention has been incorporated into the genome of the micro-organism or introduced as a part of an expression vector in a manner allowing the micro-organism to express and optionally secrete the polypeptide. In a preferred embodiment, the composition comprises at least 2 different nucleotide sequences encoding at least 2 different polypeptides of the invention. In a much preferred embodiment, the composition comprises at least 2 different nucleotide sequences encoding at least one polypeptide of the invention and at

least one polypeptide belonging to the group of ST-CF (Elhay MJ and Andersen P, Immunology and cell Biology (1997) 75, 595-603) such as ESAT-6, CFP7, CFP10, CFP17, CFP21, CFP25, CFP29, MPB59, MPT59, MPB64, and MPT64.

- 5 Individuals infected with virulent *Mycobacteria* can generally be divided into two groups. The first group has an infection with a virulent *Mycobacterium* e.g. contacts of TB patients. The virulent *Mycobacterium* may have established colonies in the lungs, but the individual has, as yet, no symptoms of TB. The second group has clinical symptoms of TB, as a TB patient.

10

In one embodiment of the invention, any of the above mentioned polypeptides are used for the manufacture of a diagnostic reagent that preferably distinguishes a subclinically or clinically infected individual (group I and group II) from an individual who has been BCG vaccinated or infected with *Mycobacterium avium* or sensitised by non-tuberculosis

- 15 *Mycobacterium* (NTM), and may distinguish a subclinically or clinically infected individual from an individual who has cleared a previous infection with a virulent *Mycobacterium*. It is most likely that specific polypeptides derived from SPE will identify group I and/or group II from individuals not infected with virulent *Mycobacteria* in the same way as ESAT-6 and CFP10 (P.Ravn et al., (1998), J. Infectious Disease 179:637-45).

20

In one embodiment of the invention, any of the above discussed polypeptides are used for the manufacture of a diagnostic reagent for the diagnosis of an infection with a virulent *Mycobacterium*. One embodiment of the invention provides a diagnostic reagent for differentiating an individual who is clinically or subclinically infected with a virulent

- 25 *Mycobacterium* from an individual not infected with virulent *Mycobacterium*, i.e. an individual who has been BCG vaccinated or infected with *Mycobacterium avium* or sensitised by non-tuberculosis *Mycobacterium* (NTM). Such a diagnostic reagent will distinguish between an individual in group I and/or II of the infection stages above, from an individual who has been vaccinated against TB. Another embodiment of the invention
- 30 provides a diagnostic reagent for differentiating an individual who is clinically or subclinically infected with a virulent *Mycobacterium* from an individual who has a cleared infection with a virulent *Mycobacterium*. Such a diagnostic reagent will distinguish between an individual in group I and/or II of the infection stages above, from an individual who has cleared the infection.

35

Determination of an infection with virulent *Mycobacterium* will be instrumental in the, still very laborious, diagnostic process of tuberculosis. A number of possible diagnostic assays and methods can be envisaged (some more specifically described in the examples and the list of properties): a sample comprising whole blood or mononuclear
5 cells (*i.a.* T-lymphocytes) from a patient could be contacted with a sample of one or more polypeptides of the invention. This contacting can be performed *in vitro* and a positive reaction could e.g. be proliferation of the T-cells or release of cytokines such as IFN- γ into the extracellular phase (e.g. into a culture supernatant).

10 Alternatively, a sample of a possibly infected organ may be contacted with an antibody raised against a polypeptide of the invention. The demonstration of the reaction by means of methods well-known in the art between the sample and the antibody will be indicative of ongoing infection and could be used to monitor treatment effect by reduction in responses. It is of course also a possibility to demonstrate the presence of anti-

15 *Mycobacterial* antibodies in serum by contacting a serum sample from a subject with at least one of the polypeptide fragments of the invention and using well-known methods for visualising the reaction between the antibody and antigen such as ELISA, Western blot, precipitation assays.

20 Also a method of determining the presence of virulent *Mycobacterium* nucleic acids in a mammal, including a human being, or in a sample, comprising incubating the sample with a nucleic acid sequence of the invention or a nucleic acid sequence complementary thereto, and detecting the presence of hybridised nucleic acids resulting from the incubation (by using the hybridisation assays which are well-known in the art), is included
25 in the invention. Such a method of diagnosing TB might involve the use of a composition comprising at least a part of a nucleotide sequence as defined above and detecting the presence of nucleotide sequences in a sample from the animal or human being to be tested which hybridises with the nucleic acid sequence (or a complementary sequence) by the use of PCR techniques.

30

The invention also relates to a method of diagnosing infection caused by a virulent *Mycobacterium* in a mammal, including a human being, comprising locally applying (patch test) or intradermally injecting (Mantoux test) a polypeptide of the invention. These tests are both called a delayed hypersensitivity reaction (DTH). A positive skin response
35 at the location of injection or application is indicative of the mammal including a human

being, being infected with a virulent *Mycobacterium*, and a negative skin response at the location of injection or application is indicative of the mammal including a human being not having TB. A positive response is a skin reaction having a diameter of at least 5 mm larger than background, but larger reactions are preferred, such as at least 1 cm, 1.5 cm, 5 and at least 2 cm in diameter. A skin reaction is here to mean erythema or induration of the skin, as directly measured. The composition used as the skin test reagent can be prepared in the same manner as described for the vaccines above.

10 In human volunteers, the generation of a significant immune response can alternatively be defined as the ability of the reagent being tested to stimulate an *in vitro* recall response by peripheral blood cells from at least 30% of PPD positive individuals previously vaccinated with that reagent or infected with a virulent *Mycobacterium*, said recall response being defined as proliferation of T cells or the production of cytokine(s) which is higher than the responses generated by cells from unimmunised or uninfected 15 control individuals, with a 95% confidence interval as defined by an appropriate statistical analysis such as a Student's two-tailed T test.

Alternatively, a significant immune response could be detected *in vivo* by a test such as the generation of delayed type hypersensitivity in the skin in response to exposure to the 20 immunising reagent, such response being significantly larger (with a 95% confidence interval as defined by appropriate statistical analysis such as a Student's two-tailed T test) in at least 30% of vaccinated or infected individuals than in placebo-treated or uninfected individuals.

25 The polypeptides according to the invention may be potential drug targets. Once a particular interesting polypeptide has been identified, the biological function of that polypeptide may be tested. The polypeptides may constitute receptor molecules or toxins which facilitates the infection by the *Mycobacterium* and if such functionality is blocked, the infectivity of the virulent *Mycobacterium* will be diminished.

30

The biological function of particular interesting polypeptides may be tested by studying the effect of inhibiting the expression of the polypeptides on the virulence of the virulent *Mycobacterium*. This inhibition may be performed at the gene level such as by blocking the expression using antisense nucleic acid, PNA or LNA or by interfering with regulatory

sequences or the inhibition may be at the level of translation or post-translational processing of the polypeptide.

Once a particular polypeptide according to the invention is identified as critical for virulence, an anti-mycobacterial agent might be designed to inhibit the expression of that polypeptide. Such anti-mycobacterial agent might be used as a prophylactic or therapeutic agent. For instance, antibodies or fragments thereof, such as Fab and (Fab')₂ fragments, can be prepared against such critical polypeptides by methods known in the art and thereafter used as prophylactic or therapeutic agents

10

A presently preferred embodiment is an extract of polypeptides obtainable by a method comprising the steps of

- a) killing a sample of virulent *Mycobacteria*;
- b) centrifugating the sample of a) at 2,000g for 40 minutes;
- 15 c) resuspending the pellet of b) in PBS and 0.5% Tween 20 and sonicating with 20 rounds of 90 seconds;
- d) centrifugating the suspension of c) at 5,000g for 30 minutes;
- e) extracting soluble proteins from the cytosol as well as cell wall and cell membrane components from the supernatant of d) with 10% SDS;
- 20 f) centrifugating the extract of e) at 20,000g for 30 minutes;
- g) precipitating the supernatant of f) with 8 volumes of cold acetone;

with an adjuvant substance.

- 25 In other words, the invention relates to use of an extract of polypeptides with an adjuvant substance for the preparation of a composition for the generation or determination of an immune response against a virulent *Mycobacterium*.

Finally, a monoclonal or polyclonal antibody, which is specifically reacting with a polypeptide of the invention in an immuno assay, or a specific binding fragment of said antibody, is also a part of the invention. The production of such polyclonal antibodies requires that a suitable animal be immunized with the polypeptide and that these antibodies are subsequently isolated, suitably by immune affinity chromatography. The production of monoclonals can be effected by methods well-known in the art, since the

30

present invention provides for adequate amounts of antigen for both immunization and screening of positive hybridomas.

Examples

EXAMPLE 1: Total extraction of proteins from dead *M.tuberculosis* bacteria.

1.5 x 10⁹ bacteria/ml *M.tuberculosis* was heat treated at 55°C for 1.5 hours and checked for sterility. 10 ml of these heat killed bacteria was centrifuged at 2000 g for 40 min; the
5 supernatant was discharged and the pellet resuspended in PBS containing 0.5% Tween 20 and used as the antigen source. The pellet was sonicated with 20 rounds of 90 seconds and centrifuged 30 min at 5000 g to remove unbroken cells. The supernatant containing soluble proteins as well as cell wall and cell membrane components was extracted twice with 10% SDS to release proteins inserted in the cell wall and membrane
10 compartments. After a centrifugation at 20.000 g for 30 min the supernatant was precipitated with 8 volume of cold acetone and resuspended in PBS at a protein concentration of 5 mg/ml and named: Somatic Proteins Extract (SPE).

Analysis of protective immune response for tuberculosis after immunisation with different *M.tuberculosis* protein preparations.

15 The protective efficacy of SPE was evaluated in a vaccination experiment and compared to the two vaccines ST-CF and BCG, known to induce protection against TB.

Five groups of 6-8 weeks old, female C57Bl/6J mice (Bomholtgaard, Denmark) were immunised subcutaneously at the base of the tail with vaccines of the following

20 composition:

Group 1: BCG

Group 2: 1x 10⁷ heat killed *M.tuberculosis*/DDA (250 µg DDA)

Group 3: 50 µg ST-CF/DDA (250 µg)

25 Group 4: 50 µg SPE/DDA (250 µg)

Group 5: Adjuvant control: DDA (250 µg) in NaCl

The animals were injected with a volume of 0.2 ml. The mice of groups 2, 3 and 4 were boosted twice at two weeks interval.

30 Four weeks after the last immunisation three mice/group were sacrificed and the spleens removed. The immune response induced in the spleen cells was monitored by release of IFN-γ into the culture supernatants when stimulated *in vitro* with relevant antigens (Table

2). ST-CF and SPE induced a similar immune response while only a very low IFN- γ release was observed after immunisation with BCG and stimulation with ST-CF.

Table 2 Recognition of protein preparations after immunisation presented as IFN- γ release (pg/ml) after restimulation.

Immunogen	No antigen	ST-CF	SPE
ST-CF	<200	6752 \pm 591	8431 \pm 459
SPE	<200	6621 \pm 203	11079 \pm 178
BCG	<200	469 \pm 32	ND

Seven weeks after the final immunisation the mice received a primary infection with 5×10^5 H37Rv in 0.1 ml iv. and two weeks later the mice were sacrificed and the spleens were isolated for bacterial enumeration (figure 2).

BCG induced a high level of protection in the spleen as expected but so did the killed H37Rv, ST-CF and SPE and all preparations induced protection at almost the same level, with SPE as the most potent of these preparations.

These data demonstrate that there are components to be found among the somatic proteins of H37Rv which in an animal model protect against tuberculosis at the same level as BCG.

EXAMPLE 2: Subcellular fractionation of *Mycobacterium tuberculosis*

1.5×10^9 colony forming units (CFU/ml) of *M. tuberculosis* H37Rv were inactivated by heat-killing at 60°C for 1.5 hour. The heat-killed Mycobacteria was centrifuged at 3,000 x g for 20 min; the supernatant was discarded and the pellet was resuspended in cold PBS. This step was repeated twice. After the final wash, the pellet was resuspended in a homogenising buffer consisting of PBS supplemented with 10 mM EDTA and 1 mM of phenylmethylsulfonyl fluoride in a ratio of 1 ml buffer per 0.5 g of heat-killed Mycobacteria. The sample was sonicated on ice for 15 min (1-min-pulser-on/10-sec-pulser off) and subsequently lysed three times with a French Pressure Cell at 12,000 lb/in². The lysate was centrifuged at 27,000 x g for 20 min; the pellet was washed in homogenising buffer and recentrifuged. The pooled supernatants contained a mixture of cytosol and membrane components, while the pellet represented the crude cell wall.

Preparation of cell wall

The cell wall pellet, resuspended in homogenising buffer, was added RNase and DNase to a final concentration of 1 mg/ml and incubated overnight at 4°C. The cell wall was washed twice in homogenising buffer, twice in homogenising buffer saturated with KCl, and twice with PBS. Soluble proteins were extracted from the cell wall by a 2 hour incubation with 2% SDS at 6°C. The insoluble cell wall core was removed by a centrifugation at 27,000 x g for 20 min and the SDS-extraction was repeated. Finally, the pooled supernatants were precipitated with 6 volumes of chilled acetone and resuspended in PBS.

10 Preparation of cytosol and membrane:

To separate the cytosol and the membrane fraction, the pooled supernatants were ultracentrifuged at 100,000 x g for 2 hours at 5°C. The cytosol proteins in the supernatant were precipitated with acetone and resuspended in PBS. The pellet, representing the membrane fraction, was washed in PBS, ultracentrifuged, and finally resuspended in PBS.

Triton X-114 extraction of cell wall and membrane:

To prepare protein fractions largely devoid of lipoarabinomannan, the cell wall and the membrane fraction were subjected to extraction with precondensed Triton X-114. Triton X-114 was added to the protein sample at a final concentration of 4%. The solution was mixed on ice for 60 min and centrifuged at 20,000 x g for 15 min at 4°C. The pellet containing residual insoluble material was extracted once more (membrane) or twice (cell wall), while the supernatant was warmed to 37°C to condense the Triton X-114. After centrifugation of the supernatant at 12,000 x g for 15 min, the aqueous phase and detergent phase were separated. The aqueous phase and detergent phase were washed twice with Triton X-114 and PBS, respectively. The combined aqueous phases and residual insoluble material containing the majority of proteins were pooled, precipitated with acetone, and resuspended in PBS.

The specificity of the human T-cell response in TB patients was investigated by stimulating PBMCs with panels of narrow molecular mass fractions from membrane, cell wall, and cytosol obtained by the multi-elution technique described by Andersen et al. (1993) J. Immunol. Methods 161:29-39. The technique resulted in 30 sharply defined fractions and allowed an identification of immunological active regions, of potential as either diagnostic reagents or as vaccine components.

The study demonstrated that multiple targets within the cell wall, membrane, and cytosol were recognised by the donors and initiated IFN- γ release as well as cellular proliferation (unpublished results). The broad cellular response were directed towards both the low molecular mass as well as the some of the higher molecular mass fractions. These
5 experiments suggest the existence of numerous target antigens among the cell wall, membrane, and cytosol fractions and it is therefore likely that some of these will have a potential as a protective or diagnostic reagent.

EXAMPLE 3: Identification of proteins from the cytosolic fraction

Use of patient sera to identify *M. tuberculosis* antigens

- 10 This example illustrates the identification of antigens from the cytosol fraction by screening with serum from *M. tuberculosis* infected individuals in western blot. The reaction with serum was used as an indication that the proteins are recognised immunologically.
- 15 The cytosol was precipitated with ammonium sulphate at 80% saturation. The non-precipitated proteins were removed by centrifugation and precipitated proteins were resuspended in 20 mM imidazole pH 7.0. The protein solution was applied to a DEAE Sepharose 6B column, equilibrated with 20 mM imidazole pH 7.0. Bound protein was eluted from the column using a salt gradient from 0 to 1 M NaCl, in 20 mM imidazole pH
20 7.0. Fractions collected during elution was analysed on a silver stained 10-20% SDS-PAGE and on 2 dimensional electrophoresis.

For use in western blot a pool of serum from 5 TB patients was made. These patients ranged from minimal to severe TB. Nitrocellulose membranes were blocked with
25 phosphate buffer, pH 7.3, containing 0.37 M NaCl and 0.5% Tween-20, for 30 min. The serum pool was diluted in phosphate buffer pH 7.3 containing 0.37 M NaCl. The blots incubated in serum dilution overnight at room temperature on a shaker. Membranes were washed for four times five minutes in the dilution buffer, and incubated with 1:1,000 diluted peroxidase-labelled swine anti human-IgG (P214, Dako) for 1 hour at room
30 temperature on a shaker. Blots were then washed for four times 5 min. in the dilution buffer and stained with DONS/TMB.

N-terminal sequencing and amino acid analysis

Proteins of the fractions containing bands reactive with serum from TB patients in Western blot were separated by 2D electrophoresis. Gels were blotted to PVDF

membranes and spots subjected to N-terminal sequencing on a Procise sequencer (Applied Biosystems).

The following N-terminal sequences were obtained :

5

For TB15 : T E R T A V L I K P D G I E R
(SEQ ID NO: 39)

For TB18 : T D T Q V T W L T Q E S H D R
(SEQ ID NO: 40)

10 For TB21 : M I D E A L F D A E E K M E K
(SEQ ID NO: 41)

For TB33 : P L P A D P S T D L S A Y A Q
(SEQ ID NO: 42)

For TB38 : M L I S Q R P T L S E D V L T
(SEQ ID NO: 43)

15

For TB54 : T G N L V T K N S L T P D V R
(SEQ ID NO: 44)

Sequence identity searches

The N-terminal sequences obtained were used for an identity search using the blast

20 program of the Sanger *M. tuberculosis* database :

http://www.sanger.ac.uk/Projects/M_tuberculosis/blast_server.shtml

In addition, the GenEMBL database was searched using the BLASTP program (Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990).

25 Basic local alignment search tool. J. Mol. Biol. 215:403-10.), to reveal proteins with homology to the full amino acid sequences obtained from the Sanger database.

Thereby, the following information was obtained :

TB15

30 For the 15 determined N-terminal amino acids for TB15 a 93% identical sequence was found in MTV008.01c. Amino acid 5 of the determined N-terminal sequence (A) is an L in the sequence MTV008.01c.

Within the open reading frame the translated protein is 136 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with the N-terminal Met cleaved off.

This gives a protein of 136 amino acids, which corresponds to a theoretical molecular mass of 14 509 Da and a theoretical pI of 5.36. The observed mass in SDS-PAGE is 14 kDa.

TB15 has 80% sequence identity in a 139 amino acid overlap to a protein of *M. smegmatis*. It is homologous to putative nucleoside diphosphate kinases from several species, e.g. 59% sequence identity to a 151 amino acid protein of *Archaeoglobus fulgidus* and 57% sequence identity to a 149 amino acid protein of *Bacillus subtilis*.

TB18

For the 15 determined N-terminal amino acids for TB18 a 100% identical sequence was found in MTCY017.33c.

15 Within the open reading frame the translated protein is 164 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with the N-terminal Met cleaved off.

This gives a protein of 164 amino acids, which corresponds to a theoretical molecular mass of 17 855 Da and a theoretical pI of 4.81. The observed mass in SDS-PAGE is 20 kDa.

TB18 has 94% sequence identity, in a 164 amino acid overlap, to a protein from *M. leprae*. In addition, it is homologous to transcription elongation factors from several species, e.g. 32% sequence identity in a 114 amino acid overlap, to a protein from *Zymomonas mobilis*.

25

TB21

For the 15 determined N-terminal amino acids for TB21 a 100% identical sequence was found in MTCY274.13c.

Within the open reading frame the translated protein is 185 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 1.

This corresponds to a theoretical molecular mass of 20 829 Da and a theoretical pI of 5.81. The observed mass in SDS-PAGE is 22 kDa.

TB21 has 90% sequence identity in a 185 amino acid overlap to a protein from *M. leprae*. In addition, it is homologous to ribosome recycling factors from several species, e.g. 63% in a 185 amino acid overlap to a protein from *Streptomyces coelicolor*.

35

TB33

For the 15 determined N-terminal amino acids for TB33 a 85% identical sequence was found in MTCY71.23. Amino acids 8 and 9 of the determined N-terminal sequence (T and

5 D) are a P and a T in MTCY71.23, respectively.

Within the open reading frame the translated protein is 297 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with the N-terminal Met cleaved off.

This gives a protein of 297 amino acids, which corresponds to a theoretical molecular
10 mass of 33 323 Da and a theoretical pI of 4.91. The observed mass in SDS-PAGE is 35 kDa.

TB33 has 83% sequence identity in a 296 amino acid overlap to a protein from *M. leprae*. In addition, it is homologous to thiosulphate sulfurtransferases (rhodanese) from several species, e.g. 48% in a 131 amino acid overlap to rhodanese from *Saccharopolyspora*

15 *erythraea*.

TB38

For the 15 determined N-terminal amino acids for TB38 a 100% identical sequence was found in MTCY13E12.10c.

Within the open reading frame the translated protein is 347 amino acids long. The N-
20 terminal sequence of the protein identified in the cytosol starts at amino acid no 1.

This corresponds to a theoretical molecular mass of 37 710 Da and a theoretical pI of 4.53. The observed mass in SDS-PAGE is 38 kDa.

TB38 is homologous to DNA-directed RNA polymerase alpha-chains from several species, e.g. 79% in a 321 amino acid overlap to a protein from *Streptomyces coelicolor*.

25

TB54

For the 15 determined N-terminal amino acids for TB54 a 100% identical sequence was found in MTCY20B11.23c.

Within the open reading frame the translated protein is 495 amino acids long. The N-
30 terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with the N-terminal Met cleaved off.

This gives a protein of 495 amino acids, which corresponds to a theoretical molecular mass of 54 329 Da and a theoretical pI of 5.00. The observed mass in SDS-PAGE is 60 kDa.

TB54 is homologous to adenosyl homocysteinases from several species, e.g. 73% in a 90 amino acid overlap to S-adenosyl-L-homocysteine hydrolase from *Triticum aestivum*. It contains a S-adenosyl-L-homocysteine hydrolase signature (PS00739).

Example 3a: Use of patient sera to identify *M. tuberculosis* cytosol antigens.

- 5 Anion exchange chromatography of the cytosol proteins and Western blot experiments with a pool of sera from TB patients were performed as described in Example 3.

N-terminal sequencing

Proteins of the fractions containing TB12.5, TB20.6, and TB40.8 were separated by 2D electrophoresis. Gels were blotted to PVDF membranes and spots subjected to N-

- 10 terminal sequencing on a Procise sequencer (Applied Biosystems).

The following N-terminal sequences were obtained :

For TB12.5 :ALKVEMVTFDXSDPA (SEQ ID NO: 80)

- 15 For TB20.6 :ADADTTDFDVDAEAP (SEQ ID NO: 81)

For TB40.8 :SKTVLILGAGVGGLT (SEQ ID NO: 82)

Sequence identity searches was performed as described in Example 3.

- 20 Thereby, the following information was obtained :

TB12.5

For the 15 determined N-terminal amino acids of TB12.5 a 93 % identical sequence was found in Rv0801. The x in position 11 is a cysteine.

- 25 Within the open reading frame the translated protein is 115 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with the N-terminal Met cleaved off.

This gives a protein of 115 amino acids, which corresponds to a theoretical molecular mass of 12 512 Da and a theoretical pI of 4.91. The observed mass in SDS-PAGE is 14

- 30 kDa.

No homology was found to TB12.5.

TB20.6

For the 15 determined N-terminal amino acids of TB20.6 a 100 % identical sequence was found in Rv3920c.

Within the open reading frame the translated protein is 187 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 1.

- 5 This gives a protein of 187 amino acids, which corresponds to a theoretical molecular mass of 20.559 Da and a theoretical pI of 4.14. The observed mass in SDS-PAGE is 24 kDa.

TB20.6 has 73 % homology to a 193 amino acid protein of *M. leprae*. It has 59% homology in a 184 amino acid overlap to a Jag-like protein from *Streptomyces coelicolor*.

10

TB40.8

For the 15 determined N-terminal amino acids of TB40.8 a 100 % identical sequence was found in Rv0331.

- 15 Within the open reading frame the translated protein is 388 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with the N-terminal Met cleaved off.

This gives a protein of 388 amino acids, which corresponds to a theoretical molecular mass of 40 792 Da and a theoretical pI of 5.06. The observed mass in SDS-PAGE is 44 kDa.

- 20 No homology was found to TB40.8.

Identification of abundant proteins

As immunity to tuberculosis is not B-cell but T-cell mediated, reactivity with serum from TB patients was not the only selection criterion used to identify proteins from the cytosol. Further proteins were selected by virtue of their abundance in the cytosol.

- 25 The cytosol was precipitated with ammonium sulphate at 80% saturation. The non-precipitated proteins were removed by centrifugation and precipitated proteins were resuspended in 20 mM imidazole, pH 7.0. The protein solution was applied to a DEAE Sepharose 6B column, equilibrated with 20 mM imidazole. Bound protein was eluted from the column using a salt gradient from 0 to 1 M NaCl, in 20 mM imidazole. Fractions
- 30 collected during elution was analyzed on a silver stained 10-20% SDS-PAGE and on 2 dimensional electrophoresis. Fractions containing well separated bands were selected for 2D electrophoresis and blotted to PVDF, after which spots, visualised by staining with Coomassie Blue, were selected for N-terminal sequencing.

- 35 The following N-terminal sequences were obtained :

For TB10C	: M E V K I G I T D S P R E L V
	(SEQ ID NO: 45)
For TB15A	: S A Y K T V V V G T D D X S X
5	(SEQ ID NO: 46)
For TB17	: M E Q R A E L V V G R A L V V
	(SEQ ID NO: 47)
For TB24	: A D I D G V T G S A G L(N) P A
	(SEQ ID NO: 48)
10 For TB27B	: T Y E T I L V E R D Q R V G I
	(SEQ ID NO: 49)

TB10C

No sequence identity was found, when searching the Sanger database using the blast
 15 program. However, when the blast program at Swiss-blast was used, a sequence was obtained.

For the 15 determined N-terminal amino acids for TB10C a 93% identical sequence was obtained. The first amino acid of the N-terminal sequence (M) is a V in the sequence found, corresponding to GTG being used as a start codon, instead of ATG.

20 Within the open reading frame the translated protein is 90 amino acids. The N-terminal sequence of the protein identified in the cytosol starts at amino acid 1.

This corresponds to a theoretical molecular mass of 9 433 Da and a theoretical pI of 4.93. The observed mass in SDS-PAGE is 10 kDa.

TB15A

25 For the determined N-terminal sequence of TB15 a 78% identical sequence was found in CY01B2.28. The X at position 13 of the determined N-terminal sequence corresponds to a G in MTCY01B2.28 and the X at position 15 to a D.

Within the open reading frame the translated protein is 146 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with
 30 the N-terminal Met cleaved off.

This gives a protein of 146 amino acids, which corresponds to a theoretical molecular mass of 15 313 Da and a theoretical pI of 5.60. The observed mass in SDS-PAGE is 16 kDa.

The highest sequence identity, 32% in a 34 amino acid overlap, was found to a conserved protein of *Methanobacterium thermoautotrophicum*.

TB17

For the 15 determined N-terminal amino acids for TB17 a 100% identical sequence was
5 found in MTV044.12.

Within the open reading frame the translated protein is 165 amino acids. The N-terminal sequence of the protein identified in the cytosol starts at amino acid 1.

This gives a protein of 165 aa. Theoretical molecular mass 16 793 Da and a theoretical pI of 4.22. The observed mass in SDS-PAGE is 18 kDa.

10 TB17 is homologous to putative molybdenum cofactor biosynthesis proteins from several species, e.g. 34% in a 103 amino acid overlap to moaCB from *Synechococcus* spp.

TB24

For the 15 determined N-terminal amino acids for TB24 a 92% identical sequence was found in MTCY07D11.03. The tentative N in position 13 of the determined amino acid
15 sequence is a Q in MTCY07D11.03, and the A at position 15 is a G.

Within the open reading frame the translated protein is 216 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with the N-terminal Met cleaved off.

This gives a protein of 216 amino acids, which corresponds to a theoretical molecular
20 mass of 24 227 Da and a theoretical pI of 4.91. The observed mass in SDS-PAGE is 28 kDa.

TB24 is homologous to a RNA polymerase sigma-E factors from several species, e.g. 55% in a 72 amino acid overlap to ECF sigma factor RpoE1 from *Myxococcus xanthus*.

TB27B

25 For the 15 determined N-terminal amino acids for TB27B a 100% identical sequence was found in MTCY017.23c.

Within the open reading frame the translated protein is 257 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with the N-terminal Met cleaved off.

30 This gives a protein of 257 amino acids, which corresponds to a theoretical molecular mass of 27 276 Da and a theoretical pI of 4.82. The observed mass in SDS-PAGE is 28 kDa.

TB27B has 86% sequence identity in a 257 amino acid overlap, to a protein from *M. leprae*. In addition, it is homologous to enoyl-CoA hydratases from several species, e.g. 66% in a 257 amino acid overlap to a protein from *Rhizobium meliloti*.

5 Identification of TB13A :

One protein spot was selected by its reaction with the monoclonal antibody ST-3 in western blot. N-terminal sequencing of the spot on the PVDF membrane corresponding to the ST-3 spot yielded the following results :

10 For TB13A : P V T Q E E I I A G I A E I I
(SEQ ID NO: 50)

Sequence identity search on the TB13A N-terminal sequence gave the following results:

15 TB13A

For the 15 determined N-terminal amino acids for TB13A a 100% identical sequence was found in MTCY427.25.

Within the open reading frame the translated protein is 115 amino acids long. The N-terminal sequence of the protein identified in the cytosol starts at amino acid no 2, with

20 the N-terminal Met cleaved off.

This gives a protein of 115 amino acids, which corresponds to a theoretical molecular mass of 12 524 Da and a theoretical pI of 3.87. The observed mass in SDS-PAGE is 10 kDa.

TB13A has 94% sequence identity to a 115 amino acid protein of *M. leprae*. It is
25 homologous to putative acyl carrier proteins from several species, e.g. 59% sequence identity to a 78 amino acid protein of *Myxococcus xanthus* and 56% to a 82 amino acid protein from *Streptomyces coelicolor*.

Identification of TB64

Biotinylated proteins were purified from the cytosol fraction in the following way: 12 mg of
30 the cytosol fraction was added to 100 µl of TetraLink Tetrameric Avidin Resin (Promega) in PBS, pH 7.4 in an eppendorf tube. After incubation over night at 4°C, centrifugation (1000 g for 5 min) was performed and the resin was washed five times with PBS, pH 7.4, each time followed by centrifugation and collection of the supernatant. Thereafter, 100 µl of 4 times concentrated SDS-PAGE sample buffer (0.08 M Tris-HCl, 8% SDS, 16%

glycerol, 24 mM EDTA , pH 8.0) was added to the resin and it was boiled for 20 minutes. After centrifugation the supernatant was collected and analysed for the presence of biotinylated proteins: The sample was analysed on SDS-PAGE followed by semi-dry blotting to nitrocellulose. The nitrocellulose membranes were incubated with alkaline phosphatase labeled streptavidin (D396, DAKO, Glostrup, Denmark). Nitro-blue tetrazolium/5-bromo-4-chloro-3-indolyl phosphate was used as substrate.

N-terminal sequencing

The eluate from the TetraLink Tetrameric Avidin Resin was loaded on a precast 10-20% Tricine SDS-PAGE gel (Novex, San Diego, USA). After electrophoresis the gel was blotted to Problott PVDF membrane (Applied Biosystems, Foster City, CA) by semidry electroblotting in 10 mM CAPS, 10% methanol, pH 11. The PVDF membrane was stained with 0.1% Coomassie R-250 in 40% methanol, 1% acetic acid, and destained in 50% methanol. A band of 10 kDa which was identified as a biotinylated protein as described above was excised and subjected to N-terminal sequence analysis by automated Edman degradation using a Procise 494 sequencer (Applied Biosystems) as described by the manufacturer.

The following sequence was obtained:

VIRRKPKPRXR

(SEQ ID NO: 57)

Submission of this sequence to the Sanger Centre *M. tuberculosis* blast server identified the open reading frame Rv3285 (91% identity in 11 amino acids) encoding a protein of 600 amino acids. The determined sequence showed identity to amino acids 511 to 521 suggesting that the identified peptide is a C-terminal fragment of the protein. As expected, the pattern for biotinylation of a lysine was identified in the C-terminal part of the protein: GDLVVLEAMKMENPVTA (residues 556-573, PROSITE pattern PS00188).

EXAMPLE 4: Identification of proteins from the cell wall.

Identification of TB11B, TB16, TB16A, TB32, TB32A, and TB51.

Proteins contained in the cell wall fraction were separated by 2-D electrophoresis. A sample containing 120 mg protein was subjected to isoelectric focusing in a pH gradient from 4 to 7. The second dimension separation (SDS-PAGE) was carried out in a 10-20% acrylamide gradient. After blotting onto a PVDF membrane, proteins could be visualised by Coomassie blue staining.

N-terminal sequencing.

The relevant spots were excised from the PVDF membrane and subjected to N-terminal sequencing using a Procise sequencer (Applied Biosystems). The following N-terminal sequences were obtained:

5		
	TB11B:PVVKINAIEVPAGA	(SEQ ID NO: 51)
	TB16:ADKTTQTIYIDADPG	(SEQ ID NO: 52)
	TB16A:PVLSKTVEVTADAAS	(SEQ ID NO: 53)
	TB32:SGNSSLGIIVGIDD	(SEQ ID NO: 54)
10	TB32A:AEVLVLVEHAEGALK	(SEQ ID NO: 55)
	TB51:MKSTVEQLSPTRVRI	(SEQ ID NO: 56)

N-terminal sequence identity searching and identification of the corresponding genes.

- The N-terminal amino acid sequence from each of the proteins identified was used for a
- 15 sequence identity search using the tblastn program at NCBI:
<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-blast?Jform=0>

The following information was obtained:

20 TB11B:

The 14 aa N-terminal sequence was found to be 100% identical to a sequence found on cosmid SCY06F7.

- The identity is found within an open reading frame of 105 amino acids length corresponding to a theoretical molecular mass of 11 185 Da and a pI of 6.18. The
- 25 apparent molecular mass in an SDS-PAGE gel is 12 kDa.

The amino acid sequence shows some low level similarity to oxygenases and hypothetical proteins.

TB16:

- The 15 aa N-terminal sequence was found to be 100% identical to a sequence found
- 30 within the Mycobacterium tuberculosis sequence MTV021.

The identity is found within an open reading frame of 144 amino acids length corresponding to a theoretical molecular mass of 16294 Da and a pI of 4.64. The apparent molecular mass in an SDS-PAGE gel is 17 kDa.

The amino acid sequence shows some similarity to other hypothetical Mycobacterial proteins.

TB16A:

The 15 aa N-terminal sequence was found to be 100% identical to a sequence found on
5 cosmid I28.

The identity is found within an open reading frame of 146 amino acids length corresponding to a theoretical molecular mass of 16 060 Da and a pI of 4.44. The apparent molecular mass in an SDS-PAGE gel is 14 kDa.

TB32:

10 The 14 aa N-terminal sequence was found to be 100% identical to a sequence found within the Mycobacterium tuberculosis sequence MTCY1A10.

The identity is found within an open reading frame of 297 amino acids length corresponding to a theoretical molecular mass of 31654 Da and a pI of 5.55. The apparent molecular mass in an SDS-PAGE gel is 33 kDa.

15 The amino acid sequence shows some similarity to other hypothetical Mycobacterial proteins.

TB32A:

The 15 aa N-terminal sequence was found to be 100% identical to a sequence found within the Mycobacterium tuberculosis sequence MTV012.

20 The identity is found within an open reading frame of 318 amino acids length corresponding to a theoretical molecular mass of 31694 Da and a pI of 4.61. The apparent molecular mass in an SDS-PAGE gel is 32 kDa.

The amino acid sequence reveals high sequence identity to the fixB gene product from several organisms. Probable electron transfer flavoprotein alpha subunit for various
25 dehydrogenases. Equivalent to Mycobacterium leprae FixB.

TB51:

The 15 aa N-terminal sequence was found to be 100% identical to a sequence found within the Mycobacterium tuberculosis sequence MTV008.

The identity is found within an open reading frame of 466 amino acids length
30 corresponding to a theoretical molecular mass of 50587 Da and a pI of 4.3. The apparent molecular mass in an SDS-PAGE gel is 56 kDa.

The amino acid sequence shows similarities to trigger factor from several organisms. Possible chaperone protein.

EXAMPLE 5: Cloning of the genes encoding TB10C, TB13A, TB17, TB11B, TB16, TB16A, TB32, TB51

The genes encoding TB10C, TB13A, TB17, TB11B, TB16, TB16A, TB32, TB51 were all cloned into the *E. coli* expression vector pMCT3, by PCR amplification with gene specific
5 primers.

Each PCR reaction contained 10 ng of *M. tuberculosis* chromosomal DNA in 1x low salt Taq+ buffer (Stratagene) supplemented with 250 μ M of each of the four nucleotides (Boehringer Mannheim), 0.5 mg/ml BSA (IgG technology), 1% DMSO (Merck), 5 pmoles of each primer, and 0.5 unit Taq+ DNA polymerase (Stratagene) in 10 μ l reaction volume.
10 Reactions were initially heated to 94°C for 25 sec. and run for 30 cycles according to the following program; 94°C for 10 sec., 55°C for 10 sec., and 72°C for 90 sec., using thermocycler equipment from Idaho Technology.

The PCR fragment was ligated with TA cloning vector pCR[®] 2.1 (Invitrogen) and transformed into *E. coli*. Plasmid DNA was thereafter prepared from clones harbouring
15 the desired fragment, digested with suitable restriction enzymes and subcloned into the expression vector pMCT3 in frame with 6 histidine residues which are added to the N-terminal of the expressed proteins. The resulting clones were hereafter sequenced by cycle sequencing using the Dye Terminator system in combination with an automated gel reader (model 373A; Applied Biosystems) according to the instructions provided. Both
20 strands of the DNA were sequenced.

Expression and metal affinity purification of recombinant proteins was undertaken essentially as described by the manufacturers. For each protein, 1 l LB-media containing 100 μ g/ml ampicillin, was inoculated with 10 ml of an overnight culture of XL1-Blue cells
25 harbouring recombinant pMCT3 plasmids. Cultures were shaken at 37°C until they reached a density of $OD_{600} = 0.4 - 0.6$. IPTG was hereafter added to a final concentration of 1 mM and the cultures were further incubated 4 - 16 hours. Cells were harvested, resuspended in 1x sonication buffer + 8 M urea and sonicated 5 x 30 sec. with 30 sec. pausing between the pulses.

30 After centrifugation, the lysate was applied to a column containing 10 ml of resuspended Talon resin (Clontec, Palo Alto, USA). The column was washed and eluted as described by the manufacturers.

After elution, all fractions (1.5 ml each) were subjected to analysis by SDS-PAGE using the Mighty Small (Hoefer Scientific Instruments, USA) system and the protein
35 concentrations were estimated at $OD_{280\text{ nm}}$. Fractions containing recombinant protein

were pooled and dialysed against 3 M urea in 10 mM Tris-HCl, pH 8.5. The dialysed protein was further purified by FPLC (Pharmacia, Sweden) using 1 ml HiTrap columns (Pharmacia, Sweden) eluted with a linear salt gradient from 0 - 1 M NaCl. Fractions were analysed by SDS-PAGE and protein concentrations were estimated at OD_{280nm}. Fractions 5 containing protein were pooled and dialysed against 25 mM Hepes buffer, pH 8.5. Finally, the protein concentration and the LPS content were determined by the BCA (Pierce, Holland) and LAL (Endosafe, Charleston, USA) tests, respectively.

For cloning of the individual proteins, the following gene specific primers were used :

10

TB10C : Primers used for cloning of TB10C :

TB10C-F : CTG AGA TCT GTG GAG GTC AAG ATC GGT (SEQ ID NO: 58)

TB10C-R : CTC CCA TGG CTAC TTA CCC GCT CGT AGC AAC (SEQ ID NO: 59)

15 TB10C-F and TB10C-R create BG/II and NcoI sites, respectively, used for the cloning in pMCT3.

TB13A : Primers used for cloning of TB13A :

20 TB13A-F : CTG AGA TCT CCT GTC ACT CAG GAA GAA (SEQ ID NO: 60)

TB13A-R : CTC CCA TGG GAA ACC GCC ATT AGC GGT (SEQ ID NO: 61)

TB13A-F and TB13A-R create BG/II and NcoI sites, respectively, used for the cloning in pMCT3.

25

TB17 : Primers used for cloning of TB17 :

TB17-F : CCC AAG CTT ATG GAA CAG CGT GCG GAG (SEQ ID NO: 62)

TB17-R : CTC CCA TGG CGA CAC TCG ATC CGG ATT (SEQ ID NO: 63)

30

TB17-F and TB17-R create BG/II and NcoI sites, respectively, used for the cloning in pMCT3.

35 TB11B : Primers used for cloning of TB11B :

TB11B-F : CTG AGA TCT ATG CCA GTG GTG AAG ATC (SEQ ID NO: 64)

TB11B-R : CTC CCA TGG TTA TGC AGT CTT GCC GGT (SEQ ID NO: 65)

TB11B-F and TB11B-R create BG/II and NcoI sites, respectively, used for the cloning in
5 pMCT3.

TB16 : Primers used for cloning OF TB16 :

TB16-F : CTG AGA TCT GCG GAC AAG ACG ACA CAG (SEQ ID NO: 66)

TB16-R : CTC CCA TGG TAC CGG AAT CAC TCA GCC (SEQ ID NO: 67)

10

TB16-F and TB16-R create BG/II and NcoI sites, respectively, used for the cloning in
pMCT3.

15 TB16A : Primers used for cloning of TB16A :

TB16A-F : CTG AGA TCT CCA GTT TTG AGC AAG ACC (SEQ ID NO: 68)

TB16A-R : CTC CCA TGG GCA CAT GCC TTA GCT GGC (SEQ ID NO: 69)

TB16A-F and TB16A-R create BG/II and NcoI sites, respectively, used for the cloning in
20 pMCT3.

TB32 : Primers used for cloning of TB32 :

TB32-F : CTG AGA TCT ATG TCA TCG GGC AAT TCA (SEQ ID NO: 70)

25 TB32-R : CTC CCA TGG CTAC CTA AGT CAG CGA CTC GCG (SEQ ID NO: 71)

TB32-F and TB32-R create BG/II and NcoI sites, respectively, used for the cloning in
pMCT3.

30

TB51 : Primers used for cloning of TB51 :

TB51-F : CTG AGA TCT GTG AAG AGC ACC GTC GAG (SEQ ID NO: 72)

TB51-R : CTC CCA TGG GTC ATA CGG TCA CGT TGT (SEQ ID NO: 73)

TB51-F and TB51-R create BG/II and NcoI sites, respectively, used for the cloning in pMCT3.

TB15A: Primers used for cloning of TB15A:

5

TB15A-F: CTG CCA TGG CTA GGT GGT GTG CAC GAT C (SEQ ID NO: 89)

TB15A-R: CTG AAG CTT ATG AGC GCC TAT AAG ACC (SEQ ID NO: 90)

10 TB15-F and TB15-R create NcoI and HindIII sites, respectively, used for the cloning in pMCT3.

TB21: Primers used for cloning of TB21:

TB21-F: CTG AGA TCT ATG ATT GAT GAGGCT CTC (SEQ ID NO: 91)

15 TB21-R: CTC CCA TGG AGC GGC CGC TAG ACC TCC (SEQ ID NO: 92)

TB21-F and TB21-R create BglII and NcoI sites, respectively, used for the cloning in pMCT3.

20 TB24: Primers used for cloning of TB24:

TB24-F: GGCTGAGACTC ATG GCC GAC ATC GAT GGT G (SEQ ID NO: 93)

TB24-R: CGTACCATGG TCA TGA CGA CAC CCC CTC GTG (SEQ ID NO: 94)

25 TB24-F and TB24-R create BglII and NcoI sites, respectively, used for the cloning in pMCT3.

TB32A: Primers used for cloning of TB32A:

30 TB32A-F: GGCTGAGACTC ATG GCT GAA GTA CTG GTG C (SEQ ID NO: 95)

TB32A-R: CGTACCATGGCTA GCC GGC GAC CGC CGG TTC (SEQ ID NO: 96)

TB32A-F and TB32A-R create BglII and NcoI sites, respectively, used for the cloning in pMCT3.

35

TB14: Primers used for cloning of TB14:

TB14-F: 5'-GTG ACC GAA CGG ACT CTG GT-3' (SEQ ID NO: 97)

TB14-R: 5'-CTA GGC GCC GGG AAA CCA GAG-3' (SEQ ID NO: 98)

5

TB18: Primers used for cloning of TB18:

TB18-F: 5'-ATG ACG GAT ACT CAA GTC ACC TG-3' (SEQ ID NO: 99)

TB18-R: 5'-GGA GTG GTA CGG CTC GGC GC-3' (SEQ ID NO: 100)

10

TB27: Primers used for cloning of TB27:

TB27-F: 5'-ATG ACG TAC GAA ACC ATC CT-3' (SEQ ID NO: 101)

TB27-R: 5'-TCA TCG GTG GGT GAA CTG GGG-3' (SEQ ID NO: 102)

15

TB33: Primers used for cloning of TB33:

TB33-F: 5'-ATG CCG CTT CCC GCA GAC CCT AG-3' (SEQ ID NO: 103)

TB33-R: 5'-TAC GAC GGG TAC CAC TCC TGG-3' (SEQ ID NO: 104)

20

TB38: Primers used for cloning of TB38:

TB38-F: 5'-ATG CTG ATC TCA CAG CGC CCC A-3' (SEQ ID NO: 105)

TB38-R: 5'-AAG CTG TTC GGT TTC GGC GTA G-3' (SEQ ID NO: 106)

25

TB54: Primers used for cloning of TB54:

TB54-F: 5' -ATG ACC GGA AAT TTG GTG AC-3' (SEQ ID NO: 107)

TB54-R: 5'-TCA GTA GCG GTA GTG GTC CGG-3' (SEQ ID NO: 108)

30

TB14, TB18, TB27, TB33, TB38 and TB54 will be cloned in ex-pressions vector pBAD-TOPO (Invitrogen).

Example 5a: Cloning of the genes encoding TB12.5, TB20.6, and TB40.8

The genes encoding TB12.5, TB20.6, and TB40.8 were all cloned into the E. coli

35 expression vector pMCT3 as described in Example 5.

For cloning of the individual genes, the following gene specific primers were used:

TB12.5: Primers used for cloning of TB12.5:

5 TB12.5-F: CTG AGA TCT ATG GCA CTC AAG GTA GAG (SEQ ID NO: 83)

TB12.5-R: CTC CCA TGG TTA TTG ACC CGC CAC GCA (SEQ ID NO: 84)

TB12.5-F and TB12.5-R create *Bgl*II and *Nco*I sites, respectively, used for the cloning in pMCT3.

10

TB20.6: Primers used for cloning of TB20.6:

TB20.6-F: CTG AGA TCT ATG GCC GAC GCT GAC ACC (SEQ ID NO: 85)

TB20.6-R: CTC CCA TGG CTA GTC GCG GAG CAC AAC. (SEQ ID NO: 86)

15 TB20.6-F and TB20.6-R create *Bgl*II and *Nco*I sites, respectively, used for the cloning in pMCT3.

TB40.8: Primers used for cloning of TB40.8:

TB40.8-F: CTG AGA TCT ATG AGC AAG ACG GTT CTC (SEQ ID NO: 87)

20 TB40.8-R: CTC CCA TGG TCA CGT CTT CCA GCG GGT (SEQ ID NO: 88)

TB40.8-F and TB40.8-R create *Bgl*II and *Nco*I sites, respectively, used for the cloning in pMCT3.

25 Expression/purification of recombinant proteins was performed as described in Example 5.

EXAMPLE 6: Evaluation of immunological activity of identified somatic proteins.

Each of the proteins identified in either the cell wall, cytosol or the cell membrane derived

30 from *M.tuberculosis* will be evaluated for the immunological recognition in *M.tuberculosis* infected animals or in TB patients.

IFN- γ induction in the mouse model of TB infection

The recognition of an antigen by IFN- γ producing T cells in *M.tuberculosis* infected animals or in TB patients is presently believed to be the most relevant correlate of protective immunity.

- 5 We will therefore evaluate the ability of the polypeptides of the invention to induce an IFN- γ production in mice of four different haplotypes during a primary infection: 8-12 weeks old female mice C57BL/6j (H-2^b), CBA/J (H-2^k), DBA.2 (H-2^d) and A.SW (H-2^s) mice (Bomholtgaard, Ry, Denmark) will be infected i.v. via the lateral tail vein with an inoculum of 5×10^4 *M.tuberculosis* suspended in PBS in a vol. of 0.1 ml. 14 days
- 10 postinfection the animals will be sacrificed and spleen cells isolated and tested for proliferation and the IFN- γ release in response to stimulation with the recombinantly produced proteins.

- As a specific model we will analyse the recognition of the purified polypeptides of the
- 15 invention the mouse model of memory immunity to TB: A group of efficiently protected mice will be generated by infecting 8-12 weeks old female C57BL/6j mice with 5×10^4 *M.tuberculosis* i.v. After 30 days of infection the mice will be subjected to 60 days of antibiotic treatment with isoniazid (Merck and Co., Rahway, NJ) and rifabutin (Farmatalia Carlo Erba, Milano, Italy) then left for 200-240 days to ensure the establishment of resting
 - 20 long-term memory immunity. Such memory immune mice are very efficient protected against a secondary infection (Orme; Andersen, Boom 1993, J.Infect.Dis. 167: 1481-1497). Long lasting immunity in this model is mediated by a population of highly reactive CD4 cells recruited to the site of infection and triggered to produce large amounts of IFN- γ in response to *M.tuberculosis* antigens.

- 25 This model will be used to identify single antigens recognised by protective T cells. Memory immune mice will be reinfected with 1×10^6 *M.tuberculosis* i.v and splenic lymphocytes harvested at day 4-6 of reinfection and proliferation and the amount of IFN- γ produced in response to any of the recombinantly produced proteins will be evaluated.

IFN- γ induction in humans during infection with virulent *Mycobacteria*.

- 30 IFN- γ is currently believed to be the best marker of protective immunity in humans. In patients with limited tuberculosis, high levels of IFN- γ can be induced, in contrast to patients with severe TB who often respond with low levels of IFN- γ (Boesen et al (1995), Human T-cell response to secreted antigen fractions of *M.tuberculosis*. Infection and Immunity 63(4):1491-1497). Furthermore, IFN- γ release has been shown to correlate

inversely with the severity of disease as determined by X-ray findings (Sodhi A, et al (1997) Clinical correlates of IFN-gamma production in patients with Tuberculosis, Clinical Infectious disease. 25; 617-620). Healthy exposed contacts of sputum positive TB patients also produce very high levels of IFN- γ in response to mycobacterial antigens (unpublished, manus in prep) indicative of early, subclinical infection. Together these findings indicate that those individuals who are relatively protected (i.e. minimal TB patients) respond with high levels of IFN- γ . The ability of the polypeptides to induce IFN- γ release in cultures of PBMC or whole blood from 20 PPD responsive patients with microscopy or culture proven TB (0-6 month after diagnosis), exposed household contacts, or BCG vaccinated individuals from different geographical regions will be evaluated. Evaluation of donors from different geographical regions will enable us to take into account the influence of i.e. exposure to virulent *Mycobacterium* or NTM (Non-Tuberculous Mycobacteria) and different genetic background. The most important selection criteria for vaccine candidates are the polypeptides which are recognised by >30% of the donors with a level of IFN γ >30% of that induced by a crude antigen preparation like ST-CF, PPD and SPE.

Cultures will be established with 1 to 2×10^5 PBMC in $200\mu\text{l}$ in microtiter plates (Nunc, Roskilde, Denmark) or with 1 ml of serum or plasma stimulated with the identified polypeptide and the IFN- γ release measured by ELISA.

Polypeptides of the invention frequently recognised will be preferred.

The use of polypeptides as diagnostic reagents:

A polypeptide has diagnostic potential in humans when it is inducing significantly higher responses in patients with microscopy or culture positive tuberculosis compared to PPD positive or PPD negative individuals with no known history of TB infection or exposure to *M.tuberculosis* but who may or may not have received a prior BCG vaccination, have been exposed to non-tuberculous mycobacteria(NTM), or be actively infected with *M.avium*. To identify polypeptides capable of discriminating between the above mentioned groups, the level of response and the frequency of positive responders to the polypeptide is compared. By positive responders are meant i) in vitro IFN- γ release by PBMC or whole blood stimulated with the polypeptide of at least $3\text{-}500$ pg/ml above background or another cut off relating to the specific test kit used, ii) reactivity by human serum or plasma from TB patients with the polypeptide using conventional antibody ELISA/Western blot or iii) in vivo delayed type hypersensitivity response to the polypeptide which is at least 5 mm higher than the response induced by a control material.

The diagnostic potential of polypeptides will initially be evaluated in 10 individuals with TB infection and 10 individuals with no known exposure to virulent Mycobacteria. High specificity, >80% ,will be the most important selection criteria for these polypeptides and
5 a sensitivity >80% is desirable but sensitivity >30% is acceptable as combinations of several specific antigens may be preferred in a cocktail of diagnostic reagent recognised by different individuals.

Skin test reaction in TB infected guinea pigs

To identify polypeptides as antigens with the potential as TB diagnostic reagents the
10 ability of the proteins to induce a skin test response will be evaluated in the guinea pig model where groups of guinea pigs have been infected with either *M.tuberculosis* or *M.avium* or vaccinated with BCG.

To evaluate the response in *M.tuberculosis* infected guinea pigs, female outbred guinea
15 pigs will be infected via an ear vein with 1×10^4 CFU of *M.tuberculosis* H37Rv in 0.2 ml of PBS or aerosol infected (in an exposure chamber of a Middlebrook Aerosol Generation device) with 1×10^5 CFU/ml of *M.tuberculosis* Erdman given rise to 10-15 granulomas per animal in the lung. After 4 weeks skin test will be performed with the polypeptides diluted in 0.1 ml of PBS and 24 hours after the injection reaction diameter is measured.

20

To evaluate the response in *M.avium* infected guinea pigs, female outbred guinea pigs will be infected intradermally with 2×10^6 CFU of a clinical isolate of *M.avium* (Atyp.1443; Statens Serum Institut, Denmark). Skin test are performed 4 weeks after with the polypeptides diluted in 0.1 ml of PBS and 24 hours after the injection reaction diameter is
25 measured.

To evaluate the response in BCG vaccinated guinea pigs, female outbred guinea pigs will be sensitized intradermally with 2×10^6 CFU of BCG (BCG Danish 1331; Statens Serum Institut). Skin test are performed 4 weeks after with the polypeptides diluted in 0.1 ml of
30 PBS and 24 hours after the injection reaction diameter is measured.

If a polypeptide induces a significant reaction in animal infected with *M.tuberculosis* but not in BCG vaccinated guinea pigs this polypeptide may have a potential as a diagnostic reagent to differentiate between BCG vaccinated and *M.tuberculosis* infected individuals,
35 which will hereafter be evaluated in the human population.

If a polypeptide induces a reaction in *M.tuberculosis* infected guinea pigs but not in guinea pigs infected with *M.avium*, this polypeptide may have a potential as a diagnostic reagent with respect to differentiate between an individual infected with *M.tuberculosis* and an individual infected with Mycobacteria not belonging to the tuberculosis complex.

- 5 The polypeptide may also have a potential as a diagnostic reagent to differentiate between a *M.avium* and a *M.tuberculosis* infected individual.

Induction of protective immunity by the recombinant proteins in the mice model.

The recombinant polypeptides will be evaluated as immunological compositions in mice.

- Female C57BL/6j mice of 6-8 weeks old (Bomholtgaard, Denmark) will be immunised subcutaneously at the base of the tail with the recombinantly produced polypeptides with DDA as adjuvant. The mice will be vaccinated with a volume of 0.2 ml in total of three times with two weeks interval between each immunisation. One week after last immunisation the mice will be bled and the blood cells isolated. The immune response induced will be monitored by release of IFN- γ into the culture supernatant when
- 15 stimulated *in vitro* with the homologous proteins.

- 6 weeks after the last immunisation the mice will be aerosol challenged with 5.5 ml of 5×10^6 viable *M.tuberculosis*/ml. After 6 weeks of infection the mice will be killed and the number of viable bacteria in lung and spleen determined by plating serial 3-fold dilution of organ homogenates on 7H11 plates. Colonies will be counted after 2-3 weeks of incubation and the levels of protection induced by each of the single polypeptide will be determined.
- 20

Example 6a: Interferon- γ induction in human TB patients and BCG vaccinated

- Human donors:** PBMC were obtained from healthy BCG vaccinated donors with no known exposure to *M. tuberculosis* and from patients with culture or microscopy proven infection with TB. Blood samples were drawn from the TB patients 0-6 months after diagnosis of tuberculosis, and 20 months to 40 years after BCG vaccination.
- 25

- Lymphocyte preparations and cell culture:** PBMC were freshly isolated by gradient centrifugation of heparinized blood on Lymphoprep (Nycomed, Oslo, Norway) and stored in liquid nitrogen until use. The cells were resuspended in complete RPMI 1640 medium (Gibco, Grand Island, N.Y.) supplemented with 1% penicillin/streptomycin (Gibco BRL, Life Technologies), 1% non-essential-amino acids (FLOW, ICN Biomedicals, CA, USA), and 10% normal human AB0 serum (NHS) from the local blood bank. The number and
- 30

the viability of the cells were determined by Nigrosin staining. Cultures were established with 1.25×10^5 PBMCs in 100 μ l in microtitre plates (Nunc, Roskilde, Denmark) and stimulated with ST-CF (5 μ g/ml), TB13A, TB15A, TB17, TB18, TB33, TB11B, TB16A, TB16, TB32, and TB51 in a final concentration of 10 μ g/ml. No antigen and
5 phytohaemagglutinin (PHA) were used as negative and positive control, respectively. Supernatants for the detection of cytokines were harvested after 5 days of culture, pooled, and stored at -80°C until used.

Cytokine analysis: Interferon- γ (IFN- γ) was detected with a standard sandwich ELISA
10 technique using a commercially available pair of monoclonal antibodies (Endogen) and used according to the manufacturers instruction. Recombinant IFN- γ (Endogen) was used as a standard. All data are means of duplicate wells and the variation between wells did not exceed 10 % of the mean. Cytokine levels below 50 pg/ml were considered negative. Responses of 10 individual donors are shown in TABLE 3.

15

As shown in Table 3, Table 4, Table 5, Table 6, Table 7, Table 8, Table 9, Table 10, Table 11, and Table 12 a marked release of IFN- γ is observed after stimulation with some of the recombinant proteins. For 50% of the donors, stimulation with TB18, TB32, and TB51 give rise to high IFN- γ responses (> 1,000 pg/ml). Less than 1/3 of the donors
20 recognised TB15A and TB11B at this level. Between 30 and 70% of the donors show intermediate IFN- γ response (> 500 pg/ml) when stimulated with TB17 and TB16A whereas only limited response was obtained by TB13A, TB33, and TB16. However, TB13A, TB33 and TB16 may still be of immunological importance and meet some of the other properties of the present invention. E.g. as demonstrated for TB33 which is
25 recognised by a pool of sera from human TB-patients.

Table 3 Stimulation of PBMCs from 6 healthy BCG vaccinated and 4 TB patients with recombinant TB13A. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml.

5 BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB13A (10 μ g/ml)
1	12	11572	10860	41
2	0	14257	11536	0
3	7	13270	8844	493
4	0	13193	2828	0
5	4	14239	14275	332
6	0	16278	12623	0

TB patients

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB13A (10 μ g/ml)
1	0	9914	3297	0
2	51	10058	6489	0
3	0	10587	9155	0
4	0	9458	5236	18

Table 4 Stimulation of PBMCs from 6 healthy BCG vaccinated and 5 TB patients with recombinant TB15A. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml.

5 BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB15A (10 μ g/ml)
1	0	18860	3733	1478
2	0	16218	2856	0
3	94	18427	13998	0
4	0	17815	4255	0
5	0	15981	10830	441
6	81	16961	11165	8009

TB patients

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB15A (10 μ g/ml)
1	231	18854	6443	57
2	0	17213	2196	0
3	0	17880	1049	0
4	0	17777	2865	0
5	0	17487	5321	0

Table 5 Stimulation of PBMCs from 6 healthy BCG vaccinated with recombinant TB17. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml

BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB17 (10 μ g/ml)
1	33	16696	7304	66
2	102	16878	6427	50
3	49	12161	11055	0
4	0	12949	2284	73
5	81	12129	6669	1029
6	0	12706	11762	656

Table 6 Stimulation of PBMCs from 3 healthy BCG vaccinated and 3 TB patients with recombinant TB18. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml

5 BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB18 (10 μ g/ml)
1	82	20862	15759	842
2	7	17785	10088	1855
3	912	16198	11350	6838

TB patients

Donor	No ag	PHA (1 μ g/ml)	ST-CF(5 μ g/ml)	TB18 (10 μ g/ml)
1	60	12301	11057	265
2	7	10390	6123	167
3	34	11678	8136	1629

Table 7 Stimulation of PBMCs from 5 healthy BCG vaccinated and 6 TB patients with recombinant TB33. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml.

5 BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB33 (10 μ g/ml)
1	589	10068	4426	721
2	1953	10817	6316	662
3	702	11837	1640	0
4	605	9463	2694	0
5	2471	7990	5979	0

TB patients

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB33 (10 μ g/ml)
1	0	3647	812	0
2	0	12266	920	0
3	0	12899	4388	0
4	0	10233	7989	0

Table 8 Stimulation of PBMCs from 3 healthy BCG vaccinated and 3 TB patients with recombinant TB11B. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml.

5 BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB11B (10 μ g/ml)
1	0	13682	9067	1379
2	0	13705	10169	2092
3	0	13231	7740	0

TB patients

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB11B (10 μ g/ml)
1	0	13285	8025	0
2	0	13157	3945	0
3	0	13207	4485	0

10 **Table 9.** Stimulation of PBMCs from 2 healthy BCG vaccinated and 5 TB patients with recombinant TB16A. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml.

BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB16A (10 μ g/ml)
1	0	12816	1831	645
2	0	14530	10293	1404

15

TB patients

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB16A (10 μ g/ml)
1	0	11606	5460	42
2	0	11836	5837	977
3	388	12353	8401	958
4	0	9587	3169	499
5	43	10820	4869	593

Table 10. Stimulation of PBMCs from 6 healthy BCG vaccinated with recombinant TB16. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml in BCG vaccinated control donors, no known TB exposure.

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB16 (10 μ g/ml)
1	33	16696	7304	0
2	102	16878	6427	292
3	49	12161	11055	514
4	0	12949	2284	24
5	81	12129	6669	58
6	0	12706	11762	36

5

Table 11. Stimulation of PBMCs from 3 healthy BCG vaccinated and 3 TB patients with recombinant TB32. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml.

10 BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB32 (10 μ g/ml)
1	82	20862	15759	1614
2	7	17785	10088	3385
3	912	16198	11350	9863

TB patients

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB32 (10 μ g/ml)
1	60	12301	11057	562
2	7	10390	6123	206
3	34	11678	8136	83

Table 12. Stimulation of PBMCs from 6 healthy BCG vaccinated with recombinant TB51. Responses to ST-CF and PHA are shown for comparison. Results are given as pg IFN- γ /ml.

5 BCG vaccinated control donors, no known TB exposure

Donor	No ag	PHA (1 μ g/ml)	ST-CF (5 μ g/ml)	TB51 (10 μ g/ml)
1	33	16696	7304	596
2	102	16878	6427	1155
3	49	12161	11055	2247
4	0	12949	2284	777
5	81	12129	6669	140
6	0	12706	11762	1123

Figure legends:**Figure 1:**

Long term protection against TB can be induced by immunisation with dead *M.tuberculosis*.

- 5 Mice received either: three immunisations with 1×10^7 CFU of dead *M.tuberculosis* H37Rv (squares); three immunisations with 50 µg of ST-CF (triangles); one immunisation with 5×10^4 CFU of live *M.tuberculosis* H37Rv (circle) and was hereafter cleared for the infection by administration of isoniazid in the drinking water. At 3, 6 and 12 month after the last immunisation the mice received an infection with *M.tuberculosis* H37Rv and two
- 10 weeks later the bacterial load and the resistance against TB in the spleens were determined.

Figure 2:

- Mice received three immunisations with 50µg of either of the three vaccines: heat killed H37Rv, SPE or ST-CF or received a vaccination with BCG. Two weeks after a primary
- 15 infection the bacterial load in the spleen was used to determined the resistance against TB.

Claims

1. A substantially pure polypeptide, which has a sequence identity of at least 80% to an amino acid sequence selected from the group consisting of SEQ ID NOs: 34, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 36, 38, 75, 77 and 79 or a subsequence of
5 at least 6 amino acids thereof, wherein the polypeptide or the subsequence thereof has at least one of the following properties:

i) the polypeptide induces an *in vitro* recall response determined by a release of IFN- γ of at least 1,500 pg/ml from reactivated memory T-lymphocytes withdrawn from a mouse
10 within 4 days after the mouse has been rechallenged with 1×10^6 virulent *Mycobacteria*, the induction being performed by the addition of the polypeptide to a suspension comprising about 2×10^5 cells isolated from the spleen of said mouse, the addition of the polypeptide resulting in a concentration of the polypeptide of not more than 20 μ g per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in
15 supernatant harvested 3 days after the addition of the polypeptide to the suspension,

ii) the polypeptide induces an *in vitro* response during primary infection with virulent *Mycobacteria*, determined by release of IFN- γ of at least 1,500 pg/ml from T-lymphocytes withdrawn from a mouse within 28 days after the mouse has been infected with 5×10^4
20 virulent *Mycobacteria*, the induction being performed by the addition of the polypeptide to a suspension comprising about 2×10^5 cells isolated from the spleen, the addition of the polypeptide resulting in a concentration of not more than 20 μ g per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 3 days after the addition of the polypeptide to the suspension,

25 iii) the polypeptide induces a protective immunity determined by vaccinating an animal with the polypeptide and an adjuvant in a total of three times with two weeks interval starting at 6-8 weeks of age, 6 weeks after the last vaccination challenging with 5×10^6 virulent *Mycobacteria*/ml by aerosol and determining a significant decrease in the number
30 of bacteria recoverable from the spleen 6 weeks after the animal has been challenged, compared to the number recovered from the same organ in an animal given placebo treatment,

iv) the polypeptide induces *in vitro* recall response determined by release of IFN- γ of at
35 least 1,000 pg/ml from Peripheral Blood Mononuclear Cells (PBMC) withdrawn from TB

patients or PPD positive individuals 0-6 months after diagnosis, the induction being performed by the addition of the polypeptide to a suspension comprising about 1.0 to 2.5×10^5 PBMC, the addition of the polypeptide resulting in a concentration of not more than $20 \mu\text{g}$ per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 5 days after the addition of the polypeptide to the suspension,

v) the polypeptide induces a specific antibody response in a TB patient as determined by an ELISA technique or a western blot when the whole blood is diluted 1:20 in PBS and stimulated with the polypeptide in a concentration of not more than $20 \mu\text{g/ml}$.

10

vi) the polypeptide induces a positive *in vitro* response determined by release of IFN- γ of at least 500 pg/ml from Peripheral Blood Mononuclear Cells (PBMC) withdrawn from an individual who is clinically or subclinically infected with a virulent *Mycobacterium*, the induction being performed by the addition of the polypeptide to a suspension comprising about 1.0 to 2.5×10^5 PBMC, the addition of the polypeptide resulting in a concentration of not more than $20 \mu\text{g}$ per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 5 days after the addition of the polypeptide to the suspension, and does not induce such an IFN- γ release in an individual not infected with a virulent *Mycobacterium*,

20

vii) the polypeptide induces a positive *in vitro* response determined by release of IFN- γ of at least 500 pg/ml from Peripheral Blood Mononuclear Cells (PBMC) withdrawn from an individual clinically or subclinically infected with a virulent *Mycobacterium*, the induction being performed by the addition of the polypeptide to a suspension comprising about 1.0 to 2.5×10^5 PBMC, the addition of the polypeptide resulting in a concentration of not more than $20 \mu\text{g}$ per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 5 days after the addition of the polypeptide to the suspension, and does not induce such a IFN- γ release in an individual who has a cleared infection with a virulent *Mycobacterium*,

30

viii) the polypeptide induces a positive DTH response determined by intradermal injection of at most $100 \mu\text{g}$ of the polypeptide to an individual who is clinically or subclinically infected with a virulent *Mycobacterium*, a positive response having a diameter of at least 10 mm 72 hours after the injection, and does not induce such a response in an individual not infected with a virulent *Mycobacterium*,

35

ix) the polypeptide induces a positive DTH response determined by intradermal injection of at most 100 µg of the polypeptide to an individual who is clinically or subclinically infected with a virulent *Mycobacterium*, a positive response having a diameter of at least 10 mm 72 hours after the injection, and does not induce such a response in an individual who has a cleared infection with a virulent *Mycobacterium*.

2. A substantially pure polypeptide which comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 34, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 36, 38, 75, 77 and 79.

3. A polypeptide according to any of claims 1 or 2, which comprises an amino acid sequence which has a sequence identity of at least 80% to an amino acid sequence selected from the group consisting of SEQ ID NOs: 34, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 36, 38, 75, 77 and 79 and/or is a subsequence thereof.

4. A purified or non-naturally occurring polypeptide as defined in any of claims 1-3 which comprises a T cell epitope.

5. A purified or non-naturally occurring polypeptide as defined in any of claims 1-4 which comprises a B cell epitope.

6. A polypeptide according to any of claims 1-5, wherein the polypeptide is encodable by a nucleic acid sequence, which sequence

25

1) is the DNA sequence selected from the group consisting of SEQ ID NOs: 33, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 74, 76, and 78 or an analogue of said sequence which hybridises with any of the DNA sequences shown in SEQ ID NOs: 33, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 74, 76, or 78 or a DNA sequence complementary thereto, or a specific part thereof, preferably under stringent hybridisation conditions, and/or

2) encodes a polypeptide, the amino acid sequence of which has a 80% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NOs: 34, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 36, 38, 75, 77 and 79 and/or

35

3) constitutes a subsequence of any of the above mentioned DNA sequences, and/or

4) constitutes a subsequence of any of the above mentioned polypeptide sequences.

5

7. A polypeptide as defined in any of claims 1-6 for use in medicine.

8. Use of a polypeptide as defined in any of claims 1-6 for the manufacture of a diagnostic reagent for the diagnosis of an infection with a virulent *Mycobacterium*.

10

9. Use of a polypeptide as defined in any of claims 1-6 for the manufacture of a composition for induction of a protective immune response in a mammal against infection with a virulent *Mycobacterium*.

15 10. A composition comprising a polypeptide as defined in any of claims 1-7, further comprising at least one other polypeptide derived from a virulent *Mycobacterium*.

11. A composition comprising, as the effective component, a micro-organism, wherein at least one copy of a DNA sequence comprising a DNA sequence encoding a polypeptide
20 as defined in any of claims 1-6 has been incorporated into the genome of the micro-organism in a manner allowing the micro-organism to express and optionally secrete the polypeptide.

12. A diagnostic reagent for diagnosing an infection with a virulent *Mycobacterium*
25 comprising a polypeptide as defined in any of claims 1-7, optionally in combination with a pharmaceutically acceptable carrier or vehicle.

13. A diagnostic reagent according to claim 12 for differentiating an individual who is clinically or subclinically infected with a virulent *Mycobacterium* from an individual not
30 infected with virulent *Mycobacterium*.

14. A diagnostic reagent according to any of claims 12 for differentiating an individual who is clinically or subclinically infected with a virulent *Mycobacterium* from an individual who has a cleared infection with a virulent *Mycobacterium*.

35

15. A diagnostic reagent according to any of claims 12 for diagnosing an infection with *Mycobacterium tuberculosis*.

16. An extract of polypeptides obtainable by a method comprising the steps of

- 5 a) killing a sample of virulent *Mycobacteria*;
b) centrifugating the sample of a) at 2,000g for 40 minutes;
c) resuspending the pellet of b) in PBS and 0.5% Tween 20 and sonicating with 20 rounds of 90 seconds;
d) centrifugating the suspension of c) at 5,000g for 30 minutes;
10 e) extracting soluble proteins from the cytosol as well as cell wall and cell membrane components from the supernatant of d) with 10% SDS;
f) centrifugating the extract of e) at 20,000g for 30 minutes;
g) precipitating the supernatant of f) with 8 volumes of cold acetone;
with an adjuvant substance.

15

17. Use of an extract of polypeptides with an adjuvant substance according to claim 16 for the preparation of a composition for the generation of an immune response against a virulent *Mycobacterium*.

- 20 18. A method of screening for inhibition of the infectivity of a virulent *Mycobacterium* belonging to the tuberculosis complex, said method comprising

a) inhibiting the expression of one or more of the polypeptides according to the invention,
and

25

b) observing the effect, if any, on the infectivity of the bacteria.

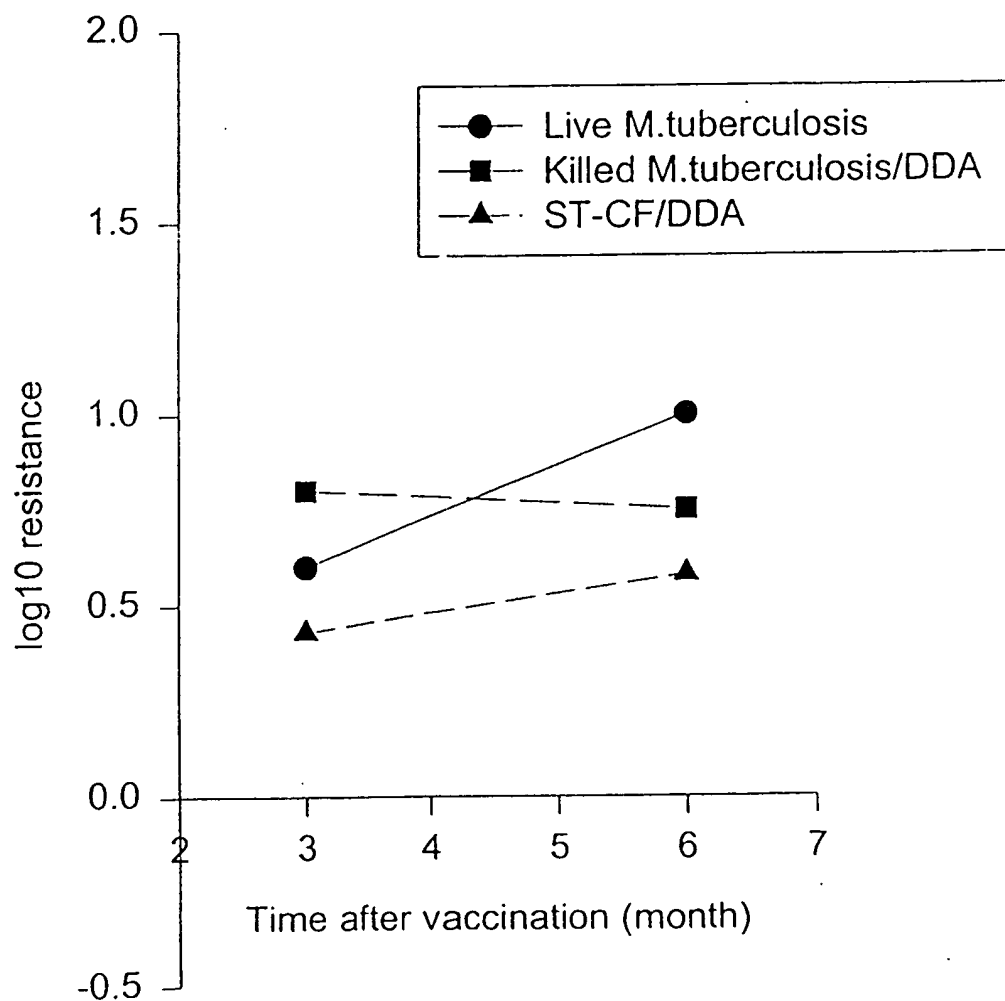
19. A method according to claim 18 wherein the expression is inhibited by blocking the transcription of the polypeptides or by interfering with regulatory sequences.

30

20. A method according to claim 19, wherein the inhibition is at the level of translation or post-translational processing of the polypeptides or by direct interaction with the polypeptides.

21. A method of using the polypeptides having a significant effect on the infectivity of a virulent *Mycobacterium* as tested in any of claims 18-20 for designing a prophylactic or therapeutic agent.
- 5 22. A nucleotide sequence which is a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 74, 76 and 78 or an analogue of said sequence which hybridises with any of the nucleotide sequences shown in SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 74, 76 or 78 or a nucleotide sequence complementary thereto, or a
10 specific part or subsequence thereof, preferably under stringent hybridisation conditions.
23. A monoclonal or polyclonal antibody, which is specifically reacting with a polypeptide according to any of claims 1-7 in an immuno assay, or a specific binding fragment of said antibody.

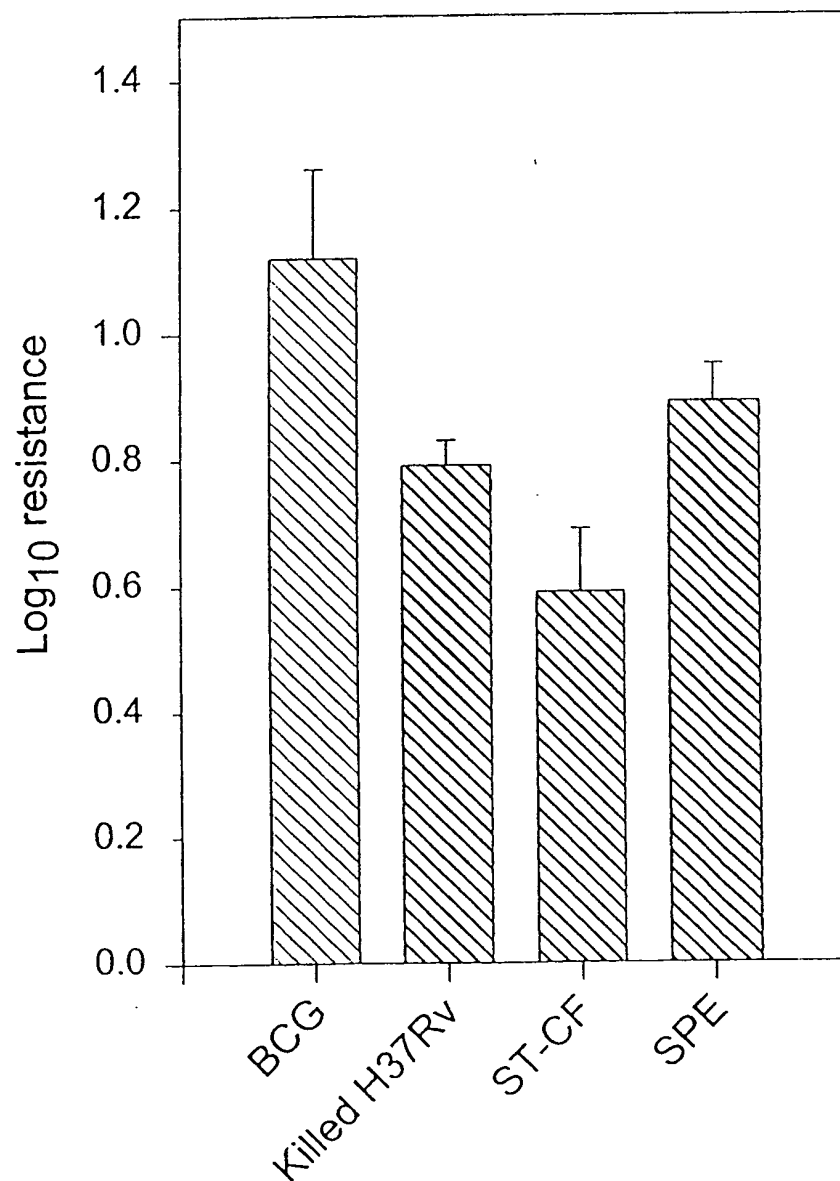
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Fig. 1**Kinetics of protective efficacy of different mycobacterial preparations**

2/2

Fig. 2

**Protective efficacy of various
bacterial preparations in the spleen**



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 gcc atc gcg gcg gtt cgc caa ctc gcc ggc ggc acc gac ccg gtg cag 288
 Ala Ile Ala Ala Val Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Gln
 85 90 95
 gcg gcg gcg ccc ggc aca atc cgg ggc gac ttc gct cta gag acg cag 336
 Ala Ala Ala Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Glu Thr Gln
 100 105 110
 ttc aac ctg gtg cac ggg tct gat tcg gcc gaa tcc gcg cag cgc gaa 384
 Phe Asn Leu Val His Gly Ser Asp Ser Ala Glu Ser Ala Gln Arg Glu
 115 120 125
 atc gcg ctc tgg ttt ccc ggc gcc tag 411
 Ile Ala Leu Trp Phe Pro Gly Ala
 130 135

<210> 6

<211> 136
 <212> PRT
 <213> M.Tuberculosis

<400> 6
 Met Thr Glu Arg Thr Leu Val Leu Ile Lys Pro Asp Gly Ile Glu Arg
 1 5 10 15
 Gln Leu Ile Gly Glu Ile Ile Ser Arg Ile Glu Arg Lys Gly Leu Thr
 20 25 30
 Ile Ala Ala Leu Gln Leu Arg Thr Val Ser Ala Glu Leu Ala Ser Gln
 35 40 45
 His Tyr Ala Glu His Glu Gly Lys Pro Phe Phe Gly Ser Leu Leu Glu
 50 55 60
 Phe Ile Thr Ser Gly Pro Val Val Ala Ala Ile Val Glu Gly Thr Arg
 65 70 75 80
 Ala Ile Ala Ala Val Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Gln
 85 90 95
 Ala Ala Ala Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Glu Thr Gln
 100 105 110
 Phe Asn Leu Val His Gly Ser Asp Ser Ala Glu Ser Ala Gln Arg Glu
 115 120 125
 Ile Ala Leu Trp Phe Pro Gly Ala
 130 135

<210> 7
 <211> 441
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(438)

<400> 7
 atg agc gcc tat aag acc gtg gtg gta gga acc gac ggt tcg gac tcg 48
 Met Ser Ala Tyr Lys Thr Val Val Val Gly Thr Asp Gly Ser Asp Ser
 1 5 10 15
 tcg atg cga gcg gta gat cgc gct gcc cag atc gcc ggc gca gac gcc 96
 Ser Met Arg Ala Val Asp Arg Ala Ala Gln Ile Ala Gly Ala Asp Ala
 20 25 30
 aag ttg atc atc gcc tcg gca tac cta cct cag cac gag gac gct cgc 144
 Lys Leu Ile Ile Ala Ser Ala Tyr Leu Pro Gln His Glu Asp Ala Arg
 35 40 45
 gcc gcc gac att ctg aag gac gaa agc tac aag gtg acg ggc acc gcc 192
 Ala Ala Asp Ile Leu Lys Asp Glu Ser Tyr Lys Val Thr Gly Thr Ala
 50 55 60
 ccg atc tac gag atc ttg cac gac gcc aag gaa cga gcg cac aac gcc 240
 Pro Ile Tyr Glu Ile Leu His Asp Ala Lys Glu Arg Ala His Asn Ala
 65 70 75 80
 ggt gcg aaa aac gtc gag gaa cgg ccg atc gtc ggc gcc ccg gtc gac 288
 Gly Ala Lys Asn Val Glu Glu Arg Pro Ile Val Gly Ala Pro Val Asp
 85 90 95
 gcg ttg gtg aac ctg gcc gat gag gag aag gcg gac ctg ctg gtc gtc 336
 Ala Leu Val Asn Leu Ala Asp Glu Glu Lys Ala Asp Leu Leu Val Val
 100 105 110

ggc aat gtc ggt ctg agc acg atc gcg ggt cgg ctg ctc gga tcg gta 384
 Gly Asn Val Gly Leu Ser Thr Ile Ala Gly Arg Leu Leu Gly Ser Val
 115 120 125

ccg gcc aat gtg tca cgc cgg gcc aag gtc gac gtg ctg atc gtg cac 432
 Pro Ala Asn Val Ser Arg Arg Ala Lys Val Asp Val Leu Ile Val His
 130 135 140

acc acc tag 441
 Thr Thr
 145

<210> 8
 <211> 146
 <212> PRT
 <213> M.Tuberculosis

<400> 8
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 1 5 10 15
 Ser Met Arg Ala Val Asp Arg Ala Ala Gln Ile Ala Gly Ala Asp Ala
 20 25 30
 Lys Leu Ile Ile Ala Ser Ala Tyr Leu Pro Gln His Glu Asp Ala Arg
 35 40 45
 Ala Ala Asp Ile Leu Lys Asp Glu Ser Tyr Lys Val Thr Gly Thr Ala
 50 55 60
 Pro Ile Tyr Glu Ile Leu His Asp Ala Lys Glu Arg Ala His Asn Ala
 65 70 75 80
 Gly Ala Lys Asn Val Glu Glu Arg Pro Ile Val Gly Ala Pro Val Asp
 85 90 95
 Ala Leu Val Asn Leu Ala Asp Glu Glu Lys Ala Asp Leu Leu Val Val
 100 105 110
 Gly Asn Val Gly Leu Ser Thr Ile Ala Gly Arg Leu Leu Gly Ser Val
 115 120 125
 Pro Ala Asn Val Ser Arg Arg Ala Lys Val Asp Val Leu Ile Val His
 130 135 140
 Thr Thr
 145

<210> 9
 <211> 498
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(495)

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 Met Glu Gln Arg Ala Glu Leu Val Val Gly Arg Ala Leu Val Val Val
 1 5 10 15

ggt gac gat cgc acg gcg cac ggc gat gaa gac cac agc ggg ccg ctt 96
 Val Asp Asp Arg Thr Ala His Gly Asp Glu Asp His Ser Gly Pro Leu
 20 25 30

gtc acc gag ctg ctc acc gag gcc ggg ttt gtt gtc gac ggc gtg gtg 144
 Val Thr Glu Leu Leu Thr Glu Ala Gly Phe Val Val Asp Gly Val Val

35	40	45	
gcg gtg tcg gcc gac gag gtc gag atc cga aat gcg ctg aac aca gcg Ala Val Ser Ala Asp Glu Val Glu Ile Arg Asn Ala Leu Asn Thr Ala 50 55 60			192
gtg atc ggc ggg gtg gac ctg gtg gtg tcg gtc ggc ggg acc ggg gtg Val Ile Gly Gly Val Asp Leu Val Val Ser Val Gly Gly Thr Gly Val 65 70 75 80			240
acg cct cgc gat gtc acc ccg gaa gcc acc cgc gac att ctg gac cgc Thr Pro Arg Asp Val Thr Pro Glu Ala Thr Arg Asp Ile Leu Asp Arg 85 90 95			288
gag atc ctc ggt atc gcc gag gcc atc cgc gcg tcc ggg ctg tcc gcg Glu Ile Leu Gly Ile Ala Glu Ala Ile Arg Ala Ser Gly Leu Ser Ala 100 105 110			336
gga atc gtc gac gcc ggg ttg tcg cgc ggc ctg gcg ggt gtc tcc ggc Gly Ile Val Asp Ala Gly Leu Ser Arg Gly Leu Ala Gly Val Ser Gly 115 120 125			384
agc acg ctg gtg gtc aac ctc gcg ggt tcg cgt tat gcg gtg cgc gat Ser Thr Leu Val Val Asn Leu Ala Gly Ser Arg Tyr Ala Val Arg Asp 130 135 140			432
gga atg gcg acg ctg aat ccg cta gcg gca cag atc atc ggg cag ttg Gly Met Ala Thr Leu Asn Pro Leu Ala Ala Gln Ile Ile Gly Gln Leu 145 150 155 160			480
tcg agc ttg gag atc tga Ser Ser Leu Glu Ile 165			498

<210> 10
 <211> 165
 <212> PRT
 <213> M.Tuberculosis

<400> 10

Met Glu Gln Arg Ala Glu Leu Val Val Gly Arg Ala Leu Val Val Val 1 5 10 15
Val Asp Asp Arg Thr Ala His Gly Asp Glu Asp His Ser Gly Pro Leu 20 25 30
Val Thr Glu Leu Leu Thr Glu Ala Gly Phe Val Val Asp Gly Val Val 35 40 45
Ala Val Ser Ala Asp Glu Val Glu Ile Arg Asn Ala Leu Asn Thr Ala 50 55 60
Val Ile Gly Gly Val Asp Leu Val Val Ser Val Gly Gly Thr Gly Val 65 70 75 80
Thr Pro Arg Asp Val Thr Pro Glu Ala Thr Arg Asp Ile Leu Asp Arg 85 90 95
Glu Ile Leu Gly Ile Ala Glu Ala Ile Arg Ala Ser Gly Leu Ser Ala 100 105 110
Gly Ile Val Asp Ala Gly Leu Ser Arg Gly Leu Ala Gly Val Ser Gly 115 120 125
Ser Thr Leu Val Val Asn Leu Ala Gly Ser Arg Tyr Ala Val Arg Asp 130 135 140
Gly Met Ala Thr Leu Asn Pro Leu Ala Ala Gln Ile Ile Gly Gln Leu 145 150 155 160

Ser Ser Leu Glu Ile
165

<210> 11
<211> 495
<212> DNA
<213> M.Tuberculosis

<220>
<221> CDS
<222> (1)...(492)

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Met Thr Asp Thr Gln Val Thr Trp Leu Thr Gln Glu Ser His Asp Arg
1 5 10 15
ctc aaa gca gag ctc gac cag ctg att gcg aat cgc ccg gtc atc gcc 96
Leu Lys Ala Glu Leu Asp Gln Leu Ile Ala Asn Arg Pro Val Ile Ala
20 25 30
gcc gaa atc aac gac cgc cgc gaa gaa ggc gac ctg cgc gag aac ggc 144
Ala Glu Ile Asn Asp Arg Arg Glu Glu Gly Asp Leu Arg Glu Asn Gly
35 40 45
gga tac cac gcc gcc cgc gag gag cag ggc cag cag gag gcc cgc att 192
Gly Tyr His Ala Ala Arg Glu Glu Gln Gly Gln Gln Glu Ala Arg Ile
50 55 60
cgc cag ctg cag gac ttg ctc agc aac gca aag gtt ggc gag gca ccc 240
Arg Gln Leu Gln Asp Leu Leu Ser Asn Ala Lys Val Gly Glu Ala Pro
65 70 75 80
aag caa tcc ggc gtc gca tta ccc ggt tct gtg gtc aag gtg tac tac 288
Lys Gln Ser Gly Val Ala Leu Pro Gly Ser Val Val Lys Val Tyr Tyr
85 90 95
aac ggc gac aag tcg gac agc gaa acg ttc ctc atc gcc acc cgc cag 336
Asn Gly Asp Lys Ser Asp Ser Glu Thr Phe Leu Ile Ala Thr Arg Gln
100 105 110
gag ggc gtc agc gac ggc aag ctc gag gtc tac tcg ccg aat tca ccg 384
Glu Gly Val Ser Asp Gly Lys Leu Glu Val Tyr Ser Pro Asn Ser Pro
115 120 125
ctc ggt ggg gcc ctg atc gac gcc aag gtc ggc gag acc cgc agc tac 432
Leu Gly Gly Ala Leu Ile Asp Ala Lys Val Gly Glu Thr Arg Ser Tyr
130 135 140
acg gtg ccc aac ggc agc acc gtg tcg gtg acc cta gtc agc gcc gag 480
Thr Val Pro Asn Gly Ser Thr Val Ser Val Thr Leu Val Ser Ala Glu
145 150 155 160
ccg tac cac tcc tag 495
Pro Tyr His Ser

<210> 12
<211> 164
<212> PRT

<213> M.Tuberculosis

<400> 12

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Met Thr Asp Thr Gln Val Thr Trp Leu Thr Gln Glu Ser His Asp Arg
 1          5          10          15
Leu Lys Ala Glu Leu Asp Gln Leu Ile Ala Asn Arg Pro Val Ile Ala
          20          25          30
Ala Glu Ile Asn Asp Arg Arg Glu Glu Gly Asp Leu Arg Glu Asn Gly
          35          40          45
Gly Tyr His Ala Ala Arg Glu Glu Gln Gly Gln Gln Glu Ala Arg Ile
          50          55          60
Arg Gln Leu Gln Asp Leu Leu Ser Asn Ala Lys Val Gly Glu Ala Pro
65          70          75          80
Lys Gln Ser Gly Val Ala Leu Pro Gly Ser Val Val Lys Val Tyr Tyr
          85          90          95
Asn Gly Asp Lys Ser Asp Ser Glu Thr Phe Leu Ile Ala Thr Arg Gln
          100          105          110
Glu Gly Val Ser Asp Gly Lys Leu Glu Val Tyr Ser Pro Asn Ser Pro
          115          120          125
Leu Gly Gly Ala Leu Ile Asp Ala Lys Val Gly Glu Thr Arg Ser Tyr
          130          135          140
Thr Val Pro Asn Gly Ser Thr Val Ser Val Thr Leu Val Ser Ala Glu
145          150          155          160
Pro Tyr His Ser

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<210> 13

<211> 558

<212> DNA

<213> M.Tuberculosis

<220>

<221> CDS

<222> (1)...(555)

<400> 13

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atg att gat gag gct ctc ttc gac gcc gaa gag aaa atg gag aag gct      48
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 1          5          10          15

gtg gcg gtg gca cgt gac gac ctg tca act atc cgt acc ggc cgc gcc      96
Val Ala Val Ala Arg Asp Asp Leu Ser Thr Ile Arg Thr Gly Arg Ala
          20          25          30

aac cct ggc atg ttc tct cgg atc acc atc gac tac tac ggt gcg gcc      144
Asn Pro Gly Met Phe Ser Arg Ile Thr Ile Asp Tyr Tyr Gly Ala Ala
          35          40          45

acc ccg atc acg caa ctg gcc agc atc aat gtc ccc gag gcg cgg cta      192
Thr Pro Ile Thr Gln Leu Ala Ser Ile Asn Val Pro Glu Ala Arg Leu
          50          55          60

gtc gtg ata aag ccg tat gaa gcc aat cag ttg cgc gct atc gag act      240
Val Val Ile Lys Pro Tyr Glu Ala Asn Gln Leu Arg Ala Ile Glu Thr
          65          70          75          80

gca att cgc aac tcc gac ctt gga gtg aat ccc acc aac gac ggc gcc      288
Ala Ile Arg Asn Ser Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Ala
          85          90          95

ctt att cgc gtg gcc gta ccg cag ctc acc gaa gaa cgt cgg cga gag      336

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Leu Ile Arg Val Ala Val Pro Gln Leu Thr Glu Glu Arg Arg Arg Glu
 100 105 110
 ctg gtc aaa cag gca aag cat aag ggg gag gag gcc aag gtt tcg gtg 384
 Leu Val Lys Gln Ala Lys His Lys Gly Glu Glu Ala Lys Val Ser Val
 115 120 125
 cgt aat atc cgt cgc aaa gcg atg gag gaa ctc cat cgc atc cgt aag 432
 Arg Asn Ile Arg Arg Lys Ala Met Glu Glu Leu His Arg Ile Arg Lys
 130 135 140
 gaa ggc gag gcc ggc gag gat gag gtc ggt cgc gca gaa aag gat ctc 480
 Glu Gly Glu Ala Gly Glu Asp Glu Val Gly Arg Ala Glu Lys Asp Leu
 145 150 155 160
 gac aag acc acg cac caa tac gtc acc caa att gat gag ctg gtt aaa 528
 Asp Lys Thr Thr His Gln Tyr Val Thr Gln Ile Asp Glu Leu Val Lys
 165 170 175
 cac aaa gaa ggc gag ctg ctg gag gtc tag 558
 His Lys Glu Gly Glu Leu Leu Glu Val
 180 185

<210> 14
 <211> 185
 <212> PRT
 <213> M.Tuberculosis

<400> 14
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 1 5 10 15
 Val Ala Val Ala Arg Asp Asp Leu Ser Thr Ile Arg Thr Gly Arg Ala
 20 25 30
 Asn Pro Gly Met Phe Ser Arg Ile Thr Ile Asp Tyr Tyr Gly Ala Ala
 35 40 45
 Thr Pro Ile Thr Gln Leu Ala Ser Ile Asn Val Pro Glu Ala Arg Leu
 50 55 60
 Val Val Ile Lys Pro Tyr Glu Ala Asn Gln Leu Arg Ala Ile Glu Thr
 65 70 75 80
 Ala Ile Arg Asn Ser Asp Leu Gly Val Asn Pro Thr Asn Asp Gly Ala
 85 90 95
 Leu Ile Arg Val Ala Val Pro Gln Leu Thr Glu Glu Arg Arg Arg Glu
 100 105 110
 Leu Val Lys Gln Ala Lys His Lys Gly Glu Glu Ala Lys Val Ser Val
 115 120 125
 Arg Asn Ile Arg Arg Lys Ala Met Glu Glu Leu His Arg Ile Arg Lys
 130 135 140
 Glu Gly Glu Ala Gly Glu Asp Glu Val Gly Arg Ala Glu Lys Asp Leu
 145 150 155 160
 Asp Lys Thr Thr His Gln Tyr Val Thr Gln Ile Asp Glu Leu Val Lys
 165 170 175
 His Lys Glu Gly Glu Leu Leu Glu Val
 180 185

<210> 15
 <211> 651
 <212> DNA
 <213> M.Tuberculosis

<220>

<221> CDS

<222> (1)...(648)

<400> 15

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Met Ala Asp Ile Asp Gly Val Thr Gly Ser Ala Gly Leu Gln Pro Gly	
1 5 10 15	
ccg tct gag gag aca gac gag gag ttg acc gcg cgt ttc gag cgc gac	96
Pro Ser Glu Glu Thr Asp Glu Glu Leu Thr Ala Arg Phe Glu Arg Asp	
20 25 30	
gcg att ccc ctg ttg gac cag ctg tac ggc ggt gcg ctg cgg atg acg	144
Ala Ile Pro Leu Leu Asp Gln Leu Tyr Gly Gly Ala Leu Arg Met Thr	
35 40 45	
cgc aat ccg gcc gac gcc gag gac ttg ctc cag gag acg atg gtg aag	192
Arg Asn Pro Ala Asp Ala Glu Asp Leu Leu Gln Glu Thr Met Val Lys	
50 55 60	
gcc tat gcg gga ttt cgt tcg ttc cgg cac ggt acc aat ctc aag gcc	240
Ala Tyr Ala Gly Phe Arg Ser Phe Arg His Gly Thr Asn Leu Lys Ala	
65 70 75 80	
tgg ctc tac cgg ata ctg acc aac acc tac atc aac agc tat cgc aag	288
Trp Leu Tyr Arg Ile Leu Thr Asn Thr Tyr Ile Asn Ser Tyr Arg Lys	
85 90 95	
aaa cag cgg caa ccg gcg gag tat ccg acc gag cag atc acc gat tgg	336
Lys Gln Arg Gln Pro Ala Glu Tyr Pro Thr Glu Gln Ile Thr Asp Trp	
100 105 110	
caa ctg gcg tcc aac gcc gag cat tcc tcg acc ggg ctg cgc tcg gct	384
Gln Leu Ala Ser Asn Ala Glu His Ser Ser Thr Gly Leu Arg Ser Ala	
115 120 125	
gaa gtc gaa gcg tta gaa gcg ttg ccg gac acc gag atc aaa gag gcg	432
Glu Val Glu Ala Leu Glu Ala Leu Pro Asp Thr Glu Ile Lys Glu Ala	
130 135 140	
ctg cag gca ttg ccg gaa gag ttc cgg atg gcg gtc tac tac gcc gat	480
Leu Gln Ala Leu Pro Glu Glu Phe Arg Met Ala Val Tyr Tyr Ala Asp	
145 150 155 160	
gtc gaa ggt ttc ccc tac aag gag atc gcc gag atc atg gat act ccg	528
Val Glu Gly Phe Pro Tyr Lys Glu Ile Ala Glu Ile Met Asp Thr Pro	
165 170 175	
atc ggc acc gtg atg tcg agg ctt cat cgc ggc cga cgt cag ttg cgc	576
Ile Gly Thr Val Met Ser Arg Leu His Arg Gly Arg Arg Gln Leu Arg	
180 185 190	
ggg ctt tta gcc gat gtg gcc agg gat cgg ggg ttt gcc agg ggc gag	624
Gly Leu Leu Ala Asp Val Ala Arg Asp Arg Gly Phe Ala Arg Gly Glu	
195 200 205	
cag gcg cac gag ggg gtg tcg tca tga	651
Gln Ala His Glu Gly Val Ser Ser	
210 215	

<210> 16
 <211> 216
 <212> PRT
 <213> M.Tuberculosis

<400> 16
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 1 5 10 15
 Pro Ser Glu Glu Thr Asp Glu Glu Leu Thr Ala Arg Phe Glu Arg Asp
 20 25 30
 Ala Ile Pro Leu Leu Asp Gln Leu Tyr Gly Gly Ala Leu Arg Met Thr
 35 40 45
 Arg Asn Pro Ala Asp Ala Glu Asp Leu Leu Gln Glu Thr Met Val Lys
 50 55 60
 Ala Tyr Ala Gly Phe Arg Ser Phe Arg His Gly Thr Asn Leu Lys Ala
 65 70 75 80
 Trp Leu Tyr Arg Ile Leu Thr Asn Thr Tyr Ile Asn Ser Tyr Arg Lys
 85 90 95
 Lys Gln Arg Gln Pro Ala Glu Tyr Pro Thr Glu Gln Ile Thr Asp Trp
 100 105 110
 Gln Leu Ala Ser Asn Ala Glu His Ser Ser Thr Gly Leu Arg Ser Ala
 115 120 125
 Glu Val Glu Ala Leu Glu Ala Leu Pro Asp Thr Glu Ile Lys Glu Ala
 130 135 140
 Leu Gln Ala Leu Pro Glu Glu Phe Arg Met Ala Val Tyr Tyr Ala Asp
 145 150 155 160
 Val Glu Gly Phe Pro Tyr Lys Glu Ile Ala Glu Ile Met Asp Thr Pro
 165 170 175
 Ile Gly Thr Val Met Ser Arg Leu His Arg Gly Arg Arg Gln Leu Arg
 180 185 190
 Gly Leu Leu Ala Asp Val Ala Arg Asp Arg Gly Phe Ala Arg Gly Glu
 195 200 205
 Gln Ala His Glu Gly Val Ser Ser
 210 215

<210> 17
 <211> 774
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(771)

<400> 17
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 1 5 10 15
 atc acg ctg aac cgt ccc cag gca ctg aac gcg ctc aac agc cag gtg 96
 Ile Thr Leu Asn Arg Pro Gln Ala Leu Asn Ala Leu Asn Ser Gln Val
 20 25 30
 atg aac gag gtc acc agc gct gca acc gaa ctg gac gat gac ccg gac 144
 Met Asn Glu Val Thr Ser Ala Ala Thr Glu Leu Asp Asp Asp Pro Asp
 35 40 45
 att ggg gcg atc atc atc acc ggt tcg gcc aaa gcg ttt gcc gcc gga 192
 Ile Gly Ala Ile Ile Ile Thr Gly Ser Ala Lys Ala Phe Ala Ala Gly
 50 55 60

gcc gac atc aaa gaa atg gcc gac ctg acg ttc gcc gac gcg ttc acc 240
 Ala Asp Ile Lys Glu Met Ala Asp Leu Thr Phe Ala Asp Ala Phe Thr
 65 70 75 80

gcc gac ttc ttc gcc acc tgg ggc aag ctg gcc gcc gtg cgc acc ccg 288
 Ala Asp Phe Phe Ala Thr Trp Gly Lys Leu Ala Ala Val Arg Thr Pro
 85 90 95

acg atc gcc gcg gtg gcg gga tac gcg ctc ggc ggt ggc tgc gag ctg 336
 Thr Ile Ala Ala Val Ala Gly Tyr Ala Leu Gly Gly Gly Cys Glu Leu
 100 105 110

gcg atg atg tgc gac gtg ctg atc gcc gcc gac acc gcg aag ttc gga 384
 Ala Met Met Cys Asp Val Leu Ile Ala Ala Asp Thr Ala Lys Phe Gly
 115 120 125

cag ccc gag ata aag ctg ggc gtg ctg cca ggc atg ggc ggc tcc cag 432
 Gln Pro Glu Ile Lys Leu Gly Val Leu Pro Gly Met Gly Gly Ser Gln
 130 135 140

cgg ctg acc cgg gct atc ggc aag gct aag gcg atg gac ctc atc ctg 480
 Arg Leu Thr Arg Ala Ile Gly Lys Ala Lys Ala Met Asp Leu Ile Leu
 145 150 155 160

acc ggg cgc acc atg gac gcc gcc gag gcc gag cgc agc ggt ctg gtt 528
 Thr Gly Arg Thr Met Asp Ala Ala Glu Ala Glu Arg Ser Gly Leu Val
 165 170 175

tca cgg gtg gtg ccg gcc gac gac ttg ctg acc gaa gcc agg gcc act 576
 Ser Arg Val Val Pro Ala Asp Asp Leu Leu Thr Glu Ala Arg Ala Thr
 180 185 190

gcc acg acc att tcg cag atg tcg gcc tcg gcg gcc cgg atg gcc aag 624
 Ala Thr Thr Ile Ser Gln Met Ser Ala Ser Ala Ala Arg Met Ala Lys
 195 200 205

gag gcc gtc aac cgg gct ttc gaa tcc agt ttg tcc gag ggg ctg ctc 672
 Glu Ala Val Asn Arg Ala Phe Glu Ser Ser Leu Ser Glu Gly Leu Leu
 210 215 220

tac gaa cgc cgg ctt ttc cat tcg gct ttc gcg acc gaa gac caa tcc 720
 Tyr Glu Arg Arg Leu Phe His Ser Ala Phe Ala Thr Glu Asp Gln Ser
 225 230 235 240

gaa ggt atg gca gcg ttc atc gag aaa cgc gct ccc cag ttc acc cac 768
 Glu Gly Met Ala Ala Phe Ile Glu Lys Arg Ala Pro Gln Phe Thr His
 245 250 255

cga tga 774
 Arg

<210> 18

<211> 257

<212> PRT

<213> M.Tuberculosis

<400> 18

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Ile Thr Leu Asn Arg Pro Gln Ala Leu Asn Ala Leu Asn Ser Gln Val
 20 25 30
 Met Asn Glu Val Thr Ser Ala Ala Thr Glu Leu Asp Asp Pro Asp
 35 40 45
 Ile Gly Ala Ile Ile Ile Thr Gly Ser Ala Lys Ala Phe Ala Ala Gly
 50 55 60
 Ala Asp Ile Lys Glu Met Ala Asp Leu Thr Phe Ala Asp Ala Phe Thr
 65 70 75 80
 Ala Asp Phe Phe Ala Thr Trp Gly Lys Leu Ala Ala Val Arg Thr Pro
 85 90 95
 Thr Ile Ala Ala Val Ala Gly Tyr Ala Leu Gly Gly Gly Cys Glu Leu
 100 105 110
 Ala Met Met Cys Asp Val Leu Ile Ala Ala Asp Thr Ala Lys Phe Gly
 115 120 125
 Gln Pro Glu Ile Lys Leu Gly Val Leu Pro Gly Met Gly Gly Ser Gln
 130 135 140
 Arg Leu Thr Arg Ala Ile Gly Lys Ala Lys Ala Met Asp Leu Ile Leu
 145 150 155 160
 Thr Gly Arg Thr Met Asp Ala Ala Glu Ala Glu Arg Ser Gly Leu Val
 165 170 175
 Ser Arg Val Val Pro Ala Asp Asp Leu Thr Glu Ala Arg Ala Thr
 180 185 190
 Ala Thr Thr Ile Ser Gln Met Ser Ala Ser Ala Ala Arg Met Ala Lys
 195 200 205
 Glu Ala Val Asn Arg Ala Phe Glu Ser Ser Leu Ser Glu Gly Leu Leu
 210 215 220
 Tyr Glu Arg Arg Leu Phe His Ser Ala Phe Ala Thr Glu Asp Gln Ser
 225 230 235 240
 Glu Gly Met Ala Ala Phe Ile Glu Lys Arg Ala Pro Gln Phe Thr His
 245 250 255
 Arg

<210> 19
 <211> 894
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(891)

<400> 19
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 Val Pro Leu Pro Ala Asp Pro Ser Pro Thr Leu Ser Ala Tyr Ala His
 1 5 10 15
 ccc gaa cgg ctc gtg acc gcc gac tgg ttg tcg gca cac atg ggc gcg 96
 Pro Glu Arg Leu Val Thr Ala Asp Trp Leu Ser Ala His Met Gly Ala
 20 25 30
 ccg ggc ctg gcg atc gtc gaa tcc gac gag gac gtc ttg ctc tac gac 144
 Pro Gly Leu Ala Ile Val Glu Ser Asp Glu Asp Val Leu Leu Tyr Asp
 35 40 45
 gtc ggc cat att ccc ggc gcc gtc aag atc gac tgg cac acc gac ctc 192
 Val Gly His Ile Pro Gly Ala Val Lys Ile Asp Trp His Thr Asp Leu
 50 55 60
 aac gac cca cgg gtg cgc gac tac atc aac ggc gag cag ttc gcc gaa 240
 Asn Asp Pro Arg Val Arg Asp Tyr Ile Asn Gly Glu Gln Phe Ala Glu

65	70	75	80	
ttg atg gac cgc aag ggc atc gcc cgc gat gac acc gtg gtg atc tat				288
Leu Met Asp Arg Lys Gly Ile Ala Arg Asp Asp Thr Val Val Ile Tyr				
	85	90	95	
ggc gac aag agc aat tgg tgg gcc gcc tat gcg ttg tgg gtg ttc acg				336
Gly Asp Lys Ser Asn Trp Trp Ala Ala Tyr Ala Leu Trp Val Phe Thr				
	100	105	110	
ctg ttc ggt cac gcc gac gtg cga ctc ctc aac ggc ggc cgt gac ctc				384
Leu Phe Gly His Ala Asp Val Arg Leu Leu Asn Gly Gly Arg Asp Leu				
	115	120	125	
tgg ctc gcc gag cgc cgg gaa acc acc ttg gac gtc ccg acc aag acc				432
Trp Leu Ala Glu Arg Arg Glu Thr Thr Leu Asp Val Pro Thr Lys Thr				
	130	135	140	
tgc acc ggt tat ccc gtc gtg cag cgc aac gat gca ccc atc cgc gca				480
Cys Thr Gly Tyr Pro Val Val Gln Arg Asn Asp Ala Pro Ile Arg Ala				
	145	150	155	160
ttc aga gac gac gtg ctg gcc atc ctg ggc gct cag ccg ctg atc gac				528
Phe Arg Asp Asp Val Leu Ala Ile Leu Gly Ala Gln Pro Leu Ile Asp				
	165	170	175	
gta cgc tct ccc gag gag tac acc ggc aag cgc acc cat atg ccc gat				576
Val Arg Ser Pro Glu Glu Tyr Thr Gly Lys Arg Thr His Met Pro Asp				
	180	185	190	
tac ccc gag gaa ggg gcg ctg cgg gcc ggt cac atc ccc acg gcg gtg				624
Tyr Pro Glu Glu Gly Ala Leu Arg Ala Gly His Ile Pro Thr Ala Val				
	195	200	205	
cac att ccg tgg ggg aag gcc gcc gac gaa agt gga cgg ttt cgc agc				672
His Ile Pro Trp Gly Lys Ala Ala Asp Glu Ser Gly Arg Phe Arg Ser				
	210	215	220	
cgc gag gaa ttg gaa cgg ctc tat gac ttc ata aac ccg gac gac caa				720
Arg Glu Glu Leu Glu Arg Leu Tyr Asp Phe Ile Asn Pro Asp Asp Gln				
	225	230	235	240
acc gtc gtc tat tgc cgc atc ggt gaa cgc tcc agc cat acc tgg ttc				768
Thr Val Val Tyr Cys Arg Ile Gly Glu Arg Ser Ser His Thr Trp Phe				
	245	250	255	
gtg ctc aca cac ctg ctg ggc aag gca gat gta cgg aac tac gac ggc				816
Val Leu Thr His Leu Leu Gly Lys Ala Asp Val Arg Asn Tyr Asp Gly				
	260	265	270	
tcg tgg acc gag tgg ggc aac gcc gtg cga gtg ccg atc gtc gcg ggc				864
Ser Trp Thr Glu Trp Gly Asn Ala Val Arg Val Pro Ile Val Ala Gly				
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gaa gaa cca gga gtg gta ccc gtc gta tga				894
Glu Glu Pro Gly Val Val Pro Val Val				
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<211> 297

<212> PRT

<213> M.Tuberculosis

<400> 20

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20      25      30
Pro Gly Leu Ala Ile Val Glu Ser Asp Glu Asp Val Leu Leu Tyr Asp
35      40      45
Val Gly His Ile Pro Gly Ala Val Lys Ile Asp Trp His Thr Asp Leu
50      55      60
Asn Asp Pro Arg Val Arg Asp Tyr Ile Asn Gly Glu Gln Phe Ala Glu
65      70      75      80
Leu Met Asp Arg Lys Gly Ile Ala Arg Asp Asp Thr Val Val Ile Tyr
85      90      95
Gly Asp Lys Ser Asn Trp Trp Ala Ala Tyr Ala Leu Trp Val Phe Thr
100     105     110
Leu Phe Gly His Ala Asp Val Arg Leu Leu Asn Gly Gly Arg Asp Leu
115     120     125
Trp Leu Ala Glu Arg Arg Glu Thr Thr Leu Asp Val Pro Thr Lys Thr
130     135     140
Cys Thr Gly Tyr Pro Val Val Gln Arg Asn Asp Ala Pro Ile Arg Ala
145     150     155     160
Phe Arg Asp Asp Val Leu Ala Ile Leu Gly Ala Gln Pro Leu Ile Asp
165     170     175
Val Arg Ser Pro Glu Glu Tyr Thr Gly Lys Arg Thr His Met Pro Asp
180     185     190
Tyr Pro Glu Glu Gly Ala Leu Arg Ala Gly His Ile Pro Thr Ala Val
195     200     205
His Ile Pro Trp Gly Lys Ala Ala Asp Glu Ser Gly Arg Phe Arg Ser
210     215     220
Arg Glu Glu Leu Glu Arg Leu Tyr Asp Phe Ile Asn Pro Asp Asp Gln
225     230     235     240
Thr Val Val Tyr Cys Arg Ile Gly Glu Arg Ser Ser His Thr Trp Phe
245     250     255
Val Leu Thr His Leu Leu Gly Lys Ala Asp Val Arg Asn Tyr Asp Gly
260     265     270
Ser Trp Thr Glu Trp Gly Asn Ala Val Arg Val Pro Ile Val Ala Gly
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Glu Glu Pro Gly Val Val Pro Val Val
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<211> 1044

<212> DNA

<213> M.Tuberculosis

<220>

<221> CDS

<222> (1)...(1041)

<400> 21

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1      5      10      15

aac cga tcc cag ttc gtg atc gaa ccg ctg gag ccg gga ttc ggc tac      96
Asn Arg Ser Gln Phe Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr
20      25      30

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acc ctg ggc aat tcg ctg cgt cgc acc ctg ctg tcg tcg att ccc gga	144
Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly	
35 40 45	
gcg gcc gtc acc agc att cgc atc gat ggt gta ctg cac gaa ttc acc	192
Ala Ala Val Thr Ser Ile Arg Ile Asp Gly Val Leu His Glu Phe Thr	
50 55 60	
acg gtg ccc ggg gtc aaa gaa gat gtc acc gag atc atc ctg aat ctc	240
Thr Val Pro Gly Val Lys Glu Asp Val Thr Glu Ile Ile Leu Asn Leu	
65 70 75 80	
aag agc ctg gtg gtg tcc tcg gag gag gac gag ccg gtc acc atg tac	288
Lys Ser Leu Val Val Ser Ser Glu Glu Asp Glu Pro Val Thr Met Tyr	
85 90 95	
cta cgc aag cag ggt ccg ggt gag gtt acc gcc ggc gac atc gtg ccg	336
Leu Arg Lys Gln Gly Pro Gly Glu Val Thr Ala Gly Asp Ile Val Pro	
100 105 110	
ccg gcc ggc gtc acc gtg cac aac ccc ggc atg cac atc gcc acg ctg	384
Pro Ala Gly Val Thr Val His Asn Pro Gly Met His Ile Ala Thr Leu	
115 120 125	
aac gat aag ggc aag ctg gaa gtc gag ctc gtc gtc gag cgt ggc cgc	432
Asn Asp Lys Gly Lys Leu Glu Val Glu Leu Val Val Glu Arg Gly Arg	
130 135 140	
ggc tat gtc ccg gcg gtg caa aac cgg gct tcg ggt gcc gaa att ggg	480
Gly Tyr Val Pro Ala Val Gln Asn Arg Ala Ser Gly Ala Glu Ile Gly	
145 150 155 160	
cgc att cca gtc gat tcc atc tac tca ccg gtg ctc aaa gtg acc tac	528
Arg Ile Pro Val Asp Ser Ile Tyr Ser Pro Val Leu Lys Val Thr Tyr	
165 170 175	
aag gtg gac gcc acc cgg gtc gag cag cgc acc gac ttc gac aag ctg	576
Lys Val Asp Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu	
180 185 190	
atc ctg gac gtg gag acc aag aat tca atc agc ccg cgc gac gcg ctg	624
Ile Leu Asp Val Glu Thr Lys Asn Ser Ile Ser Pro Arg Asp Ala Leu	
195 200 205	
gcg tcg gct ggc aag acg ctg gtc gag ttg ttc ggc ctg gca cgg gaa	672
Ala Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu	
210 215 220	
ctc aac gtc gag gcc gaa ggc atc gag atc ggg ccg tcg ccg gcc gag	720
Leu Asn Val Glu Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Ala Glu	
225 230 235 240	
gcc gat cac att gcg tca ttc gcc ctg ccg atc gac gac ctg gat ctg	768
Ala Asp His Ile Ala Ser Phe Ala Leu Pro Ile Asp Asp Leu Asp Leu	
245 250 255	
acg gtg cgg tcc tac aac tgc ctc aag cgc gag ggg gtg cac acc gtg	816
Thr Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Gly Val His Thr Val	
260 265 270	
ggc gaa ctg gtg gcg cgc acc gaa tcc gac ctg ctt gac atc cgc aac	864

Gly	Glu	Leu	Val	Ala	Arg	Thr	Glu	Ser	Asp	Leu	Leu	Asp	Ile	Arg	Asn		
		275					280					285					
ttc	ggt	cag	aag	tcc	atc	gac	gag	gtg	aag	atc	aag	ctg	cac	cag	ctg	912	
Phe	Gly	Gln	Lys	Ser	Ile	Asp	Glu	Val	Lys	Ile	Lys	Leu	His	Gln	Leu		
	290					295					300						
ggc	ctg	tca	ctc	aag	gac	agc	ccg	ccg	agc	ttc	gac	ccc	tcg	gag	gtc	960	
Gly	Leu	Ser	Leu	Lys	Asp	Ser	Pro	Pro	Ser	Phe	Asp	Pro	Ser	Glu	Val		
305					310					315					320		
gcg	ggc	tac	gac	gtc	gcc	acc	ggc	acc	tgg	tcg	acc	gag	ggc	gcg	tac	1008	
Ala	Gly	Tyr	Asp	Val	Ala	Thr	Gly	Thr	Trp	Ser	Thr	Glu	Gly	Ala	Tyr		
				325					330					335			
gac	gag	cag	gac	tac	gcc	gaa	acc	gaa	cag	ctt	tag					1044	
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<211> 347

<212> PRT

<213> M.Tuberculosis

<400> 22

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			20					25					30				
Thr	Leu	Gly	Asn	Ser	Leu	Arg	Arg	Thr	Leu	Leu	Ser	Ser	Ile	Pro	Gly		
		35					40					45					
Ala	Ala	Val	Thr	Ser	Ile	Arg	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Thr		
	50					55					60						
Thr	Val	Pro	Gly	Val	Lys	Glu	Asp	Val	Thr	Glu	Ile	Ile	Leu	Asn	Leu		
65					70					75					80		
Lys	Ser	Leu	Val	Val	Ser	Ser	Glu	Glu	Asp	Glu	Pro	Val	Thr	Met	Tyr		
			85						90					95			
Leu	Arg	Lys	Gln	Gly	Pro	Gly	Glu	Val	Thr	Ala	Gly	Asp	Ile	Val	Pro		
			100					105					110				
Pro	Ala	Gly	Val	Thr	Val	His	Asn	Pro	Gly	Met	His	Ile	Ala	Thr	Leu		
		115					120					125					
Asn	Asp	Lys	Gly	Lys	Leu	Glu	Val	Glu	Leu	Val	Val	Glu	Arg	Gly	Arg		
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Gly	Tyr	Val	Pro	Ala	Val	Gln	Asn	Arg	Ala	Ser	Gly	Ala	Glu	Ile	Gly		
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Arg	Ile	Pro	Val	Asp	Ser	Ile	Tyr	Ser	Pro	Val	Leu	Lys	Val	Thr	Tyr		
				165					170					175			
Lys	Val	Asp	Ala	Thr	Arg	Val	Glu	Gln	Arg	Thr	Asp	Phe	Asp	Lys	Leu		
			180					185					190				
Ile	Leu	Asp	Val	Glu	Thr	Lys	Asn	Ser	Ile	Ser	Pro	Arg	Asp	Ala	Leu		
		195					200					205					
Ala	Ser	Ala	Gly	Lys	Thr	Leu	Val	Glu	Leu	Phe	Gly	Leu	Ala	Arg	Glu		
		210				215					220						
Leu	Asn	Val	Glu	Ala	Glu	Gly	Ile	Glu	Ile	Gly	Pro	Ser	Pro	Ala	Glu		
225					230					235					240		
Ala	Asp	His	Ile	Ala	Ser	Phe	Ala	Leu	Pro	Ile	Asp	Asp	Leu	Asp	Leu		
				245					250					255			
Thr	Val	Arg	Ser	Tyr	Asn	Cys	Leu	Lys	Arg	Glu	Gly	Val	His	Thr	Val		
				260				265					270				
Gly	Glu	Leu	Val	Ala	Arg	Thr	Glu	Ser	Asp	Leu	Leu	Asp	Ile	Arg	Asn		

275	280	285
Phe Gly Gln Lys Ser Ile Asp Glu Val Lys Ile Lys Leu His Gln Leu		
290	295	300
Gly Leu Ser Leu Lys Asp Ser Pro Pro Ser Phe Asp Pro Ser Glu Val		
305	310	315
Ala Gly Tyr Asp Val Ala Thr Gly Thr Trp Ser Thr Glu Gly Ala Tyr		
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Asp Glu Gln Asp Tyr Ala Glu Thr Glu Gln Leu		
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aac ggc atc gac ttt aag atc gcc gac ctg tca cta gcg gat ttc ggc	96
Asn Gly Ile Asp Phe Lys Ile Ala Asp Leu Ser Leu Ala Asp Phe Gly	
20 25 30	
cgc aaa gaa ctc cgg atc gcc gag cac gag atg ccc ggc ctg atg tcg	144
Arg Lys Glu Leu Arg Ile Ala Glu His Glu Met Pro Gly Leu Met Ser	
35 40 45	
ctg cgg cgc gag tat gcc gag gtg caa ccc ctg aag ggg gcc cgg atc	192
Leu Arg Arg Glu Tyr Ala Glu Val Gln Pro Leu Lys Gly Ala Arg Ile	
50 55 60	
tcg ggt tcg ctg cac atg acg gtg cag acc gcg gtg ttg atc gaa acc	240
Ser Gly Ser Leu His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr	
65 70 75 80	
ctc acc gcg ctg ggc gcc gaa gtc cgc tgg gcc tcg tgc aac atc ttc	288
Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe	
85 90 95	
tcc acc cag gat cac gcc gcc gcc gcc gtc gtg gtc ggc ccg cac ggc	336
Ser Thr Gln Asp His Ala Ala Ala Ala Val Val Val Gly Pro His Gly	
100 105 110	
acc ccc gac gag ccc aag ggt gtc ccg gtg ttc gcg tgg aag ggc gag	384
Thr Pro Asp Glu Pro Lys Gly Val Pro Val Phe Ala Trp Lys Gly Glu	
115 120 125	
acg ctc gaa gag tac tgg tgg gcc gcc gag cag atg ctc acc tgg ccg	432
Thr Leu Glu Glu Tyr Trp Trp Ala Ala Glu Gln Met Leu Thr Trp Pro	
130 135 140	
gac ccc gac aag ccg gcc aac atg atc ctc gat gac ggc ggt gac gcc	480
Asp Pro Asp Lys Pro Ala Asn Met Ile Leu Asp Asp Gly Gly Asp Ala	
145 150 155 160	
acc atg ttg gtg ctg cgc gcc atg cag tat gag aag gcc ggc gtg gtg	528

Thr	Met	Leu	Val	Leu	Arg	Gly	Met	Gln	Tyr	Glu	Lys	Ala	Gly	Val	Val		
				165					170					175			
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Pro	Pro	Ala	Glu	Glu	Asp	Asp	Pro	Ala	Glu	Trp	Lys	Val	Phe	Leu	Asn		
			180					185					190				
ctg	cta	cgg	acc	cgc	ttc	gag	acc	gac	aag	gac	aag	tgg	acc	aag	ata	624	
Leu	Leu	Arg	Thr	Arg	Phe	Glu	Thr	Asp	Lys	Asp	Lys	Trp	Thr	Lys	Ile		
			195				200					205					
gcc	gag	tcg	gtc	aag	ggc	gtc	acc	gag	gag	acc	acc	acc	ggc	gtg	ctg	672	
Ala	Glu	Ser	Val	Lys	Gly	Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	Leu		
	210					215				220							
cgg	ctc	tac	caa	ttc	gcc	gcg	gcc	ggg	gat	ctg	gcc	ttc	ccg	gcg	atc	720	
Arg	Leu	Tyr	Gln	Phe	Ala	Ala	Ala	Gly	Asp	Leu	Ala	Phe	Pro	Ala	Ile		
225					230				235						240		
aac	gtc	aac	gac	tcg	gtg	acc	aag	tcc	aaa	ttc	gac	aac	aag	tac	ggc	768	
Asn	Val	Asn	Asp	Ser	Val	Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly		
				245				250						255			
act	cgg	cac	tcc	ctg	atc	gac	ggc	atc	aac	cgc	ggc	acc	gac	gcg	ctg	816	
Thr	Arg	His	Ser	Leu	Ile	Asp	Gly	Ile	Asn	Arg	Gly	Thr	Asp	Ala	Leu		
			260					265					270				
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Ile	Gly	Gly	Lys	Lys	Val	Leu	Ile	Cys	Gly	Tyr	Gly	Asp	Val	Gly	Lys		
		275					280					285					
ggc	tgt	gcg	gag	gcg	atg	aag	ggc	cag	gga	gcg	cgg	gtc	tcc	gtc	acc	912	
Gly	Cys	Ala	Glu	Ala	Met	Lys	Gly	Gln	Gly	Ala	Arg	Val	Ser	Val	Thr		
	290					295					300						
gag	atc	gac	ccg	atc	aac	gcg	ctg	cag	gcc	atg	atg	gag	ggc	ttc	gac	960	
Glu	Ile	Asp	Pro	Ile	Asn	Ala	Leu	Gln	Ala	Met	Met	Glu	Gly	Phe	Asp		
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gtg	gtc	acc	gtc	gag	gag	gcc	atc	ggg	gac	gcc	gac	atc	gtc	gta	acc	1008	
Val	Val	Thr	Val	Glu	Glu	Ala	Ile	Gly	Asp	Ala	Asp	Ile	Val	Val	Thr		
				325					330					335			
gcg	acc	ggc	aac	aaa	gac	atc	atc	atg	ctc	gag	cac	att	aag	gcg	atg	1056	
Ala	Thr	Gly	Asn	Lys	Asp	Ile	Ile	Met	Leu	Glu	His	Ile	Lys	Ala	Met		
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Lys	Asp	His	Ala	Ile	Leu	Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile		
			355				360					365					
gac	atg	gcc	ggg	ctg	gag	cgc	tcc	ggg	gcg	aca	cgg	gtc	aac	gtc	aag	1152	
Asp	Met	Ala	Gly	Leu	Glu	Arg	Ser	Gly	Ala	Thr	Arg	Val	Asn	Val	Lys		
	370					375					380						
cct	cag	gtc	gac	ctg	tgg	acc	ttt	ggc	gac	acg	ggc	cgc	tcg	atc	atc	1200	
Pro	Gln	Val	Asp	Leu	Trp	Thr	Phe	Gly	Asp	Thr	Gly	Arg	Ser	Ile	Ile		
385					390				395						400		
gtg	ctg	tcc	gag	ggg	cgg	ctg	ctg	aac	ctg	ggc	aat	gcc	acc	ggg	cac	1248	
Val	Leu	Ser	Glu	Gly	Arg	Leu	Leu	Asn	Leu	Gly	Asn	Ala	Thr	Gly	His		

405	410	415	
ccc tcg ttc gtg atg agc aac agc ttc gct aac cag acg atc gcc cag			1296
Pro Ser Phe Val Met Ser Asn Ser Phe Ala Asn Gln Thr Ile Ala Gln			
420	425	430	
atc gag ctg tgg acc aag aac gac gag tac gac aac gag gtg tac cgg			1344
Ile Glu Leu Trp Thr Lys Asn Asp Glu Tyr Asp Asn Glu Val Tyr Arg			
435	440	445	
ctg ccc aag cac ctc gac gag aag gtg gct cga atc cat gtc gag gcc			1392
Leu Pro Lys His Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala			
450	455	460	
ctt ggc ggt cac ctg acc aag ctg acc aag gag cag gcc gaa tac ctc			1440
Leu Gly Gly His Leu Thr Lys Leu Thr Lys Glu Gln Ala Glu Tyr Leu			
465	470	475	480
ggc gtc gac gtc gag ggt ccc tac aag ccg gac cac tac cgc tac			1485
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485	490	495	
tga			1488
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Arg Lys Glu Leu Arg Ile Ala Glu His Glu Met Pro Gly Leu Met Ser			
35	40	45	
Leu Arg Arg Glu Tyr Ala Glu Val Gln Pro Leu Lys Gly Ala Arg Ile			
50	55	60	
Ser Gly Ser Leu His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr			
65	70	75	80
Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe			
85	90	95	
Ser Thr Gln Asp His Ala Ala Ala Val Val Val Gly Pro His Gly			
100	105	110	
Thr Pro Asp Glu Pro Lys Gly Val Pro Val Phe Ala Trp Lys Gly Glu			
115	120	125	
Thr Leu Glu Glu Tyr Trp Trp Ala Ala Glu Gln Met Leu Thr Trp Pro			
130	135	140	
Asp Pro Asp Lys Pro Ala Asn Met Ile Leu Asp Asp Gly Gly Asp Ala			
145	150	155	160
Thr Met Leu Val Leu Arg Gly Met Gln Tyr Glu Lys Ala Gly Val Val			
165	170	175	
Pro Pro Ala Glu Asp Asp Pro Ala Glu Trp Lys Val Phe Leu Asn			
180	185	190	
Leu Leu Arg Thr Arg Phe Glu Thr Asp Lys Asp Lys Trp Thr Lys Ile			
195	200	205	
Ala Glu Ser Val Lys Gly Val Thr Glu Glu Thr Thr Gly Val Leu			
210	215	220	
Arg Leu Tyr Gln Phe Ala Ala Ala Gly Asp Leu Ala Phe Pro Ala Ile			
225	230	235	240
Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly			

21

				245					250					255			
Thr	Arg	His	Ser	Leu	Ile	Asp	Gly	Ile	Asn	Arg	Gly	Thr	Asp	Ala	Leu		
			260					265					270				
Ile	Gly	Gly	Lys	Lys	Val	Leu	Ile	Cys	Gly	Tyr	Gly	Asp	Val	Gly	Lys		
		275					280					285					
Gly	Cys	Ala	Glu	Ala	Met	Lys	Gly	Gln	Gly	Ala	Arg	Val	Ser	Val	Thr		
	290					295					300						
Glu	Ile	Asp	Pro	Ile	Asn	Ala	Leu	Gln	Ala	Met	Met	Glu	Gly	Phe	Asp		
305					310					315					320		
Val	Val	Thr	Val	Glu	Glu	Ala	Ile	Gly	Asp	Ala	Asp	Ile	Val	Val	Thr		
			325						330						335		
Ala	Thr	Gly	Asn	Lys	Asp	Ile	Ile	Met	Leu	Glu	His	Ile	Lys	Ala	Met		
			340					345					350				
Lys	Asp	His	Ala	Ile	Leu	Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile		
	355						360					365					
Asp	Met	Ala	Gly	Leu	Glu	Arg	Ser	Gly	Ala	Thr	Arg	Val	Asn	Val	Lys		
	370					375					380						
Pro	Gln	Val	Asp	Leu	Trp	Thr	Phe	Gly	Asp	Thr	Gly	Arg	Ser	Ile	Ile		
385					390					395					400		
Val	Leu	Ser	Glu	Gly	Arg	Leu	Leu	Asn	Leu	Gly	Asn	Ala	Thr	Gly	His		
			405						410					415			
Pro	Ser	Phe	Val	Met	Ser	Asn	Ser	Phe	Ala	Asn	Gln	Thr	Ile	Ala	Gln		
			420					425						430			
Ile	Glu	Leu	Trp	Thr	Lys	Asn	Asp	Glu	Tyr	Asp	Asn	Glu	Val	Tyr	Arg		
	435					440						445					
Leu	Pro	Lys	His	Leu	Asp	Glu	Lys	Val	Ala	Arg	Ile	His	Val	Glu	Ala		
	450				455						460						
Leu	Gly	Gly	His	Leu	Thr	Lys	Leu	Thr	Lys	Glu	Gln	Ala	Glu	Tyr	Leu		
465					470					475					480		
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<211> 1803

<212> DNA

<213> M.Tuberculosis

<220>

<221> CDS

<222> (1)...(1800)

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Val	Ala	Ser	His	Ala	Gly	Ser	Arg	Ile	Ala	Arg	Ile	Ser	Lys	Val	Leu		
1				5					10					15			
gtc	gcc	aat	cgc	ggc	gag	atc	gca	gtg	cgg	gtg	atc	cgg	gcg	gcc	cgc		96
Val	Ala	Asn	Arg	Gly	Glu	Ile	Ala	Val	Arg	Val	Ile	Arg	Ala	Ala	Arg		
			20					25					30				
gac	gcc	ggc	ctg	ccc	agc	gtg	gcg	gtg	tac	gcc	gaa	ccc	gac	gcc	gag		144
Asp	Ala	Gly	Leu	Pro	Ser	Val	Ala	Val	Tyr	Ala	Glu	Pro	Asp	Ala	Glu		
		35					40					45					
tcc	ccg	cat	gtt	cgg	ctg	gcc	gac	gag	gcg	ttc	gcg	ctg	ggc	ggc	cag		192
Ser	Pro	His	Val	Arg	Leu	Ala	Asp	Glu	Ala	Phe	Ala	Leu	Gly	Gly	Gln		
	50					55					60						
acc	tcg	gcg	gag	tcc	tat	ctg	gac	ttc	gcc	aag	atc	ctc	gac	gcg	gca		240
Thr	Ser	Ala	Glu	Ser	Tyr	Leu	Asp	Phe	Ala	Lys	Ile	Leu	Asp	Ala	Ala		
	65				70					75					80		

gcc aag tcc ggg gcc aac gcc atc cac ccc ggc tac ggc ttc cta gcg Ala Lys Ser Gly Ala Asn Ala Ile His Pro Gly Tyr Gly Phe Leu Ala 85 90 95	288
gaa aat gcc gac ttc gcc cag gcg gtg atc gac gcc ggc ctg atc tgg Glu Asn Ala Asp Phe Ala Gln Ala Val Ile Asp Ala Gly Leu Ile Trp 100 105 110	336
atc ggc ccc agc ccg cag tcg atc cgc gac ctg ggc gac aag gtc acg Ile Gly Pro Ser Pro Gln Ser Ile Arg Asp Leu Gly Asp Lys Val Thr 115 120 125	384
gcc cgt cac atc gcg gcc cgc gct cag gcg ccc ctg gtg ccg ggt acc Ala Arg His Ile Ala Ala Arg Ala Gln Ala Pro Leu Val Pro Gly Thr 130 135 140	432
ccc gat ccg gtc aaa ggc gcc gac gag gtg gtg gca ttc gcc gag gag Pro Asp Pro Val Lys Gly Ala Asp Glu Val Val Ala Phe Ala Glu Glu 145 150 155 160	480
tac ggc ctg ccg atc gcg atc aag gcc gcc cac ggc ggc ggc ggc aag Tyr Gly Leu Pro Ile Ala Ile Lys Ala Ala His Gly Gly Gly Gly Lys 165 170 175	528
ggc atg aag gtg gcc cgc acc atc gac gag att ccg gag ctg tac gag Gly Met Lys Val Ala Arg Thr Ile Asp Glu Ile Pro Glu Leu Tyr Glu 180 185 190	576
tcg gcg gtg cgc gag gcc acg gcc gcg ttc ggc cgc ggt gag tgc tac Ser Ala Val Arg Glu Ala Thr Ala Ala Phe Gly Arg Gly Glu Cys Tyr 195 200 205	624
gtg gag cgc tat ctc gac aag ccg cgc cac gtc gaa gca cag gtg atc Val Glu Arg Tyr Leu Asp Lys Pro Arg His Val Glu Ala Gln Val Ile 210 215 220	672
gcc gac cag cac ggc aac gtc gtc gtc gcc ggc acc ccg gac tgc tcg Ala Asp Gln His Gly Asn Val Val Val Ala Gly Thr Arg Asp Cys Ser 225 230 235 240	720
ctg cag cgc cgc tac cag aag ctg gtc gag gag gcg ccc gca ccg ttc Leu Gln Arg Arg Tyr Gln Lys Leu Val Glu Glu Ala Pro Ala Pro Phe 245 250 255	768
ctg acc gac ttt caa cgc aaa gag atc cac gac tcg gcc aaa ccg att Leu Thr Asp Phe Gln Arg Lys Glu Ile His Asp Ser Ala Lys Arg Ile 260 265 270	816
tgc aaa gag gcc cat tac cac ggc gcc ggc acc gtc gaa tac ctg gtc Cys Lys Glu Ala His Tyr His Gly Ala Gly Thr Val Glu Tyr Leu Val 275 280 285	864
ggt cag gac ggc ttg atc tcg ttc ttg gag gtc aac acg cgc ctt cag Gly Gln Asp Gly Leu Ile Ser Phe Leu Glu Val Asn Thr Arg Leu Gln 290 295 300	912
gta gaa cac ccg gtc acc gag gaa acc gcg ggc atc gac ttg gtg ctg Val Glu His Pro Val Thr Glu Glu Thr Ala Gly Ile Asp Leu Val Leu 305 310 315 320	960

cag	caa	ttc	cgg	atc	gcc	aac	ggc	gaa	aag	ctg	gac	atc	acc	gag	gat	1008
Gln	Gln	Phe	Arg	Ile	Ala	Asn	Gly	Glu	Lys	Leu	Asp	Ile	Thr	Glu	Asp	
			325						330					335		
ccc	acc	ccg	cgc	ggg	cac	gcc	atc	gaa	ttc	cgg	atc	aac	ggc	gag	gac	1056
Pro	Thr	Pro	Arg	Gly	His	Ala	Ile	Glu	Phe	Arg	Ile	Asn	Gly	Glu	Asp	
			340					345					350			
gcg	ggg	cgt	aac	ttc	cta	ccg	gcg	ccc	ggg	ccg	gtg	aca	aag	ttc	cac	1104
Ala	Gly	Arg	Asn	Phe	Leu	Pro	Ala	Pro	Gly	Pro	Val	Thr	Lys	Phe	His	
			355				360					365				
ccg	ccg	tcc	ggc	ccc	ggt	gtg	cgg	gtg	gac	tcc	ggt	gtc	gag	acc	ggc	1152
Pro	Pro	Ser	Gly	Pro	Gly	Val	Arg	Val	Asp	Ser	Gly	Val	Glu	Thr	Gly	
		370				375					380					
tcg	gtg	atc	ggc	ggc	cag	ttc	gac	tcg	atg	ctg	gcc	aag	ctg	atc	gtg	1200
Ser	Val	Ile	Gly	Gly	Gln	Phe	Asp	Ser	Met	Leu	Ala	Lys	Leu	Ile	Val	
385					390					395					400	
cac	ggt	gcc	gac	cgc	gcc	gag	gcg	ctg	gcg	cgg	gcc	cgg	cgc	gcg	ctg	1248
His	Gly	Ala	Asp	Arg	Ala	Glu	Ala	Leu	Ala	Arg	Ala	Arg	Arg	Ala	Leu	
			405					410						415		
aac	gag	ttc	ggt	gtc	gaa	ggc	ctg	gcg	acg	gtc	atc	ccg	ttt	cac	cgc	1296
Asn	Glu	Phe	Gly	Val	Glu	Gly	Leu	Ala	Thr	Val	Ile	Pro	Phe	His	Arg	
			420				425						430			
gcc	gtg	gtg	tcc	gac	ccg	gca	ttc	atc	ggc	gac	gcg	aac	ggc	ttt	tcg	1344
Ala	Val	Val	Ser	Asp	Pro	Ala	Phe	Ile	Gly	Asp	Ala	Asn	Gly	Phe	Ser	
			435				440					445				
gta	cat	acc	cgc	tgg	atc	gag	acc	gag	tgg	aat	aac	acc	atc	gag	ccc	1392
Val	His	Thr	Arg	Trp	Ile	Glu	Thr	Glu	Trp	Asn	Asn	Thr	Ile	Glu	Pro	
		450				455					460					
ttt	acc	gac	ggc	gaa	cct	ctc	gac	gag	gac	gcc	cgg	ccg	cgt	cag	aag	1440
Phe	Thr	Asp	Gly	Glu	Pro	Leu	Asp	Glu	Asp	Ala	Arg	Pro	Arg	Gln	Lys	
465					470					475					480	
gtg	gtc	gtc	gaa	atc	gac	ggt	cgc	cgc	gtc	gaa	gtc	tcg	ctg	ccg	gct	1488
Val	Val	Val	Glu	Ile	Asp	Gly	Arg	Arg	Val	Glu	Val	Ser	Leu	Pro	Ala	
			485						490					495		
gat	ctc	gcg	ctg	tcc	aat	ggc	ggc	ggt	tgc	gac	ccg	gtc	ggt	gtc	atc	1536
Asp	Leu	Ala	Leu	Ser	Asn	Gly	Gly	Gly	Cys	Asp	Pro	Val	Gly	Val	Ile	
			500					505					510			
cgg	cgc	aag	ccc	aag	ccg	cgc	aag	cgg	ggt	gcg	cac	acc	ggc	gcg	gcg	1584
Arg	Arg	Lys	Pro	Lys	Pro	Arg	Lys	Arg	Gly	Ala	His		Gly	Ala	Ala	
		515					520					525				
gcc	tcc	ggt	gac	gcg	gtg	acc	gcg	cct	atg	cag	ggc	acc	gta	gtt	aag	1632
Ala	Ser	Gly	Asp	Ala	Val	Thr	Ala	Pro	Met	Gln	Gly	Thr	Val	Val	Lys	
		530				535					540					
ttc	gcg	gtc	gaa	gaa	ggg	caa	gag	gtc	gtg	gcc	ggc	gac	cta	gtg	gtg	1680
Phe	Ala	Val	Glu	Glu	Gly	Gln	Glu	Val	Val	Ala	Gly	Asp	Leu	Val	Val	
545					550					555					560	
gtc	ctc	gag	gcg	atg	aag	atg	gaa	aac	ccg	gtc	acc	gcg	cat	aag	gat	1728

Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Thr Ala His Lys Asp
 565 570 575

ggc acc atc acc ggg ctg gcg gtc gag gcg ggc gcg gcc atc acc cag 1776
 Gly Thr Ile Thr Gly Leu Ala Val Glu Ala Gly Ala Ala Ile Thr Gln
 580 585 590

ggc acg gtg ctc gcc gag atc aag taa 1803
 Gly Thr Val Leu Ala Glu Ile Lys
 595 600

<210> 26
 <211> 600
 <212> PRT
 <213> M.Tuberculosis

<400> 26
 Val Ala Ser His Ala Gly Ser Arg Ile Ala Arg Ile Ser Lys Val Leu
 1 5 10 15
 Val Ala Asn Arg Gly Glu Ile Ala Val Arg Val Ile Arg Ala Ala Arg
 20 25 30
 Asp Ala Gly Leu Pro Ser Val Ala Val Tyr Ala Glu Pro Asp Ala Glu
 35 40 45
 Ser Pro His Val Arg Leu Ala Asp Glu Ala Phe Ala Leu Gly Gly Gln
 50 55 60
 Thr Ser Ala Glu Ser Tyr Leu Asp Phe Ala Lys Ile Leu Asp Ala Ala
 65 70 75 80
 Ala Lys Ser Gly Ala Asn Ala Ile His Pro Gly Tyr Gly Phe Leu Ala
 85 90 95
 Glu Asn Ala Asp Phe Ala Gln Ala Val Ile Asp Ala Gly Leu Ile Trp
 100 105 110
 Ile Gly Pro Ser Pro Gln Ser Ile Arg Asp Leu Gly Asp Lys Val Thr
 115 120 125
 Ala Arg His Ile Ala Ala Arg Ala Gln Ala Pro Leu Val Pro Gly Thr
 130 135 140
 Pro Asp Pro Val Lys Gly Ala Asp Glu Val Val Ala Phe Ala Glu Glu
 145 150 155 160
 Tyr Gly Leu Pro Ile Ala Ile Lys Ala Ala His Gly Gly Gly Gly Lys
 165 170 175
 Gly Met Lys Val Ala Arg Thr Ile Asp Glu Ile Pro Glu Leu Tyr Glu
 180 185 190
 Ser Ala Val Arg Glu Ala Thr Ala Ala Phe Gly Arg Gly Glu Cys Tyr
 195 200 205
 Val Glu Arg Tyr Leu Asp Lys Pro Arg His Val Glu Ala Gln Val Ile
 210 215 220
 Ala Asp Gln His Gly Asn Val Val Val Ala Gly Thr Arg Asp Cys Ser
 225 230 235 240
 Leu Gln Arg Arg Tyr Gln Lys Leu Val Glu Glu Ala Pro Ala Pro Phe
 245 250 255
 Leu Thr Asp Phe Gln Arg Lys Glu Ile His Asp Ser Ala Lys Arg Ile
 260 265 270
 Cys Lys Glu Ala His Tyr His Gly Ala Gly Thr Val Glu Tyr Leu Val
 275 280 285
 Gly Gln Asp Gly Leu Ile Ser Phe Leu Glu Val Asn Thr Arg Leu Gln
 290 295 300
 Val Glu His Pro Val Thr Glu Glu Thr Ala Gly Ile Asp Leu Val Leu
 305 310 315 320
 Gln Gln Phe Arg Ile Ala Asn Gly Glu Lys Leu Asp Ile Thr Glu Asp
 325 330 335
 Pro Thr Pro Arg Gly His Ala Ile Glu Phe Arg Ile Asn Gly Glu Asp

340 345 350
 Ala Gly Arg Asn Phe Leu Pro Ala Pro Gly Pro Val Thr Lys Phe His
 355 360 365
 Pro Pro Ser Gly Pro Gly Val Arg Val Asp Ser Gly Val Glu Thr Gly
 370 375 380
 Ser Val Ile Gly Gly Gln Phe Asp Ser Met Leu Ala Lys Leu Ile Val
 385 390 395 400
 His Gly Ala Asp Arg Ala Glu Ala Leu Ala Arg Ala Arg Arg Ala Leu
 405 410 415
 Asn Glu Phe Gly Val Glu Gly Leu Ala Thr Val Ile Pro Phe His Arg
 420 425 430
 Ala Val Val Ser Asp Pro Ala Phe Ile Gly Asp Ala Asn Gly Phe Ser
 435 440 445
 Val His Thr Arg Trp Ile Glu Thr Glu Trp Asn Asn Thr Ile Glu Pro
 450 455 460
 Phe Thr Asp Gly Glu Pro Leu Asp Glu Asp Ala Arg Pro Arg Gln Lys
 465 470 475 480
 Val Val Val Glu Ile Asp Gly Arg Arg Val Glu Val Ser Leu Pro Ala
 485 490 495
 Asp Leu Ala Leu Ser Asn Gly Gly Gly Cys Asp Pro Val Gly Val Ile
 500 505 510
 Arg Arg Lys Pro Lys Pro Arg Lys Arg Gly Ala His Thr Gly Ala Ala
 515 520 525
 Ala Ser Gly Asp Ala Val Thr Ala Pro Met Gln Gly Thr Val Val Lys
 530 535 540
 Phe Ala Val Glu Glu Gly Gln Glu Val Val Ala Gly Asp Leu Val Val
 545 550 555 560
 Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Thr Ala His Lys Asp
 565 570 575
 Gly Thr Ile Thr Gly Leu Ala Val Glu Ala Gly Ala Ala Ile Thr Gln
 580 585 590
 Gly Thr Val Leu Ala Glu Ile Lys
 595 600

<210> 27

<211> 318

<212> DNA

<213> M.Tuberculosis

<220>

<221> CDS

<222> (1)... (315)

<400> 27

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Met Pro Val Val Lys Ile Asn Ala Ile Glu Val Pro Ala Gly Ala Gly	
1 5 10 15	
ccc gag ctg gag aag cgg ttc gct cac cgc gcg cac gcg gtc gag aac	96
Pro Glu Leu Glu Lys Arg Phe Ala His Arg Ala His Ala Val Glu Asn	
20 25 30	
tcc ccg ggt ttc ctc ggc ttt cag ctg tta cgt ccg gtc aag ggt gaa	144
Ser Pro Gly Phe Leu Gly Phe Gln Leu Leu Arg Pro Val Lys Gly Glu	
35 40 45	
gaa cgc tac ttc gtg gtg aca cac tgg gag tcc gat gaa gca ttc cag	192
Glu Arg Tyr Phe Val Val Thr His Trp Glu Ser Asp Glu Ala Phe Gln	
50 55 60	
gcg tgg gca aac ggg ccc gcc atc gca gcc cat gcc gga cac cgg gcc	240

Ala Trp Ala Asn Gly Pro Ala Ile Ala Ala His Ala Gly His Arg Ala
 65 70 75 80

aac ccc gtg gcg acc ggt gct tcg ctg ctg gaa ttc gag gtc gtg ctt 288
 Asn Pro Val Ala Thr Gly Ala Ser Leu Leu Glu Phe Glu Val Val Leu
 85 90 95

gac gtc ggt ggg acc ggc aag act gca taa 318
 Asp Val Gly Gly Thr Gly Lys Thr Ala
 100 105

<210> 28
 <211> 105
 <212> PRT
 <213> M.Tuberculosis

<400> 28

Met Pro Val Val Lys Ile Asn Ala Ile Glu Val Pro Ala Gly Ala Gly
 1 5 10 15

Pro Glu Leu Glu Lys Arg Phe Ala His Arg Ala His Ala Val Glu Asn
 20 25 30

Ser Pro Gly Phe Leu Gly Phe Gln Leu Leu Arg Pro Val Lys Gly Glu
 35 40 45

Glu Arg Tyr Phe Val Val Thr His Trp Glu Ser Asp Glu Ala Phe Gln
 50 55 60

Ala Trp Ala Asn Gly Pro Ala Ile Ala Ala His Ala Gly His Arg Ala
 65 70 75 80

Asn Pro Val Ala Thr Gly Ala Ser Leu Leu Glu Phe Glu Val Val Leu
 85 90 95

Asp Val Gly Gly Thr Gly Lys Thr Ala
 100 105

<210> 29
 <211> 435
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(435)

<400> 29

gtg gcg gac aag acg aca cag acg att tac atc gac gcg gat cca ggc 48
 Val Ala Asp Lys Thr Thr Gln Thr Ile Tyr Ile Asp Ala Asp Pro Gly
 1 5 10 15

gag gtg atg aag gcg atc gcc gac atc gaa gcc tac ccg caa tgg att 96
 Glu Val Met Lys Ala Ile Ala Asp Ile Glu Ala Tyr Pro Gln Trp Ile
 20 25 30

tcg gag tat aag gaa gtc gag atc cta gag gcc gac gac gag ggc tac 144
 Ser Glu Tyr Lys Glu Val Glu Ile Leu Glu Ala Asp Asp Glu Gly Tyr
 35 40 45

ccg aaa cga gcg cga atg ttg atg gac gca gcc atc ttc aaa gac acc 192
 Pro Lys Arg Ala Arg Met Leu Met Asp Ala Ala Ile Phe Lys Asp Thr
 50 55 60

ttg atc atg tcc tac gag tgg ccg gaa gac cgc caa tcg ctt agc tgg 240
 Leu Ile Met Ser Tyr Glu Trp Pro Glu Asp Arg Gln Ser Leu Ser Trp

65	70	75	80	
act ctc gaa tcc agc tcg ctg cta aag tcc ctc gaa ggc acg tat cgc				288
Thr Leu Glu Ser Ser Ser Leu Leu Lys Ser Leu Glu Gly Thr Tyr Arg				
	85	90	95	
ttg gcg ccc aag ggt tct ggc act gag gtc acc tac gag ctt gcc gtc				336
Leu Ala Pro Lys Gly Ser Gly Thr Glu Val Thr Tyr Glu Leu Ala Val				
	100	105	110	
gac ctt gct gtc ccc atg atc ggg atg ctc aag cgt aag gcg gaa cgc				384
Asp Leu Ala Val Pro Met Ile Gly Met Leu Lys Arg Lys Ala Glu Arg				
	115	120	125	
agg ttg ata gac ggc gcg ttg aag gat ctg aag aaa cga gtc gag ggc				432
Arg Leu Ile Asp Gly Ala Leu Lys Asp Leu Lys Lys Arg Val Glu Gly				
	130	135	140	
tga				435
*				

<210> 30
 <211> 144
 <212> PRT
 <213> M.Tuberculosis

<400> 30
 Met Ala Asp Lys Thr Thr Gln Thr Ile Tyr Ile Asp Ala Asp Pro Gly
 1 5 10 15
 Glu Val Met Lys Ala Ile Ala Asp Ile Glu Ala Tyr Pro Gln Trp Ile
 20 25 30
 Ser Glu Tyr Lys Glu Val Glu Ile Leu Glu Ala Asp Asp Glu Gly Tyr
 35 40 45
 Pro Lys Arg Ala Arg Met Leu Met Asp Ala Ala Ile Phe Lys Asp Thr
 50 55 60
 Leu Ile Met Ser Tyr Glu Trp Pro Glu Asp Arg Gln Ser Leu Ser Trp
 65 70 75 80
 Thr Leu Glu Ser Ser Ser Leu Leu Lys Ser Leu Glu Gly Thr Tyr Arg
 85 90 95
 Leu Ala Pro Lys Gly Ser Gly Thr Glu Val Thr Tyr Glu Leu Ala Val
 100 105 110
 Asp Leu Ala Val Pro Met Ile Gly Met Leu Lys Arg Lys Ala Glu Arg
 115 120 125
 Arg Leu Ile Asp Gly Ala Leu Lys Asp Leu Lys Lys Arg Val Glu Gly
 130 135 140

<210> 31
 <211> 441
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(438)

<400> 31
 atg cca gtt ttg agc aag acc gtc gag gtc acc gcc gac gcc gca tcg
 Met Pro Val Leu Ser Lys Thr Val Glu Val Thr Ala Asp Ala Ala Ser
 1 5 10 15

atc atg gcc atc gtt gcc gat atc gag cgc tac cca gag tgg aat gaa 96
 Ile Met Ala Ile Val Ala Asp Ile Glu Arg Tyr Pro Glu Trp Asn Glu
 20 25 30

 ggg gtc aag ggc gca tgg gtg ctc gct cgc tac gat gac ggg cgt ccc 144
 Gly Val Lys Gly Ala Trp Val Leu Ala Arg Tyr Asp Asp Gly Arg Pro
 35 40 45

 agc cag gtg cgg ctc gac acc gct gtt caa ggc atc gag ggc acc tat 192
 Ser Gln Val Arg Leu Asp Thr Ala Val Gln Gly Ile Glu Gly Thr Tyr
 50 55 60

 atc cac gcc gtg tac tac cca ggc gaa aac cag att caa acc gtc atg 240
 Ile His Ala Val Tyr Tyr Pro Gly Glu Asn Gln Ile Gln Thr Val Met
 65 70 75 80

 cag cag ggt gaa ctg ttt gcc aag cag gag cag ctg ttc agt gtg gtg 288
 Gln Gln Gly Glu Leu Phe Ala Lys Gln Glu Gln Leu Phe Ser Val Val
 85 90 95

 gca acc ggc gcc gcg agc ttg ctc acg gtg gac atg gac gtc cag gtc 336
 Ala Thr Gly Ala Ala Ser Leu Leu Thr Val Asp Met Asp Val Gln Val
 100 105 110

 acc atg ccg gtg ccc gag ccg atg gtg aag atg ctg ctc aac aac gtc 384
 Thr Met Pro Val Pro Glu Pro Met Val Lys Met Leu Leu Asn Asn Val
 115 120 125

 ctg gag cat ctc gcc gaa aat ctc aag cag cgc gcc gag cag ctg gcg 432
 Leu Glu His Leu Ala Glu Asn Leu Lys Gln Arg Ala Glu Gln Leu Ala
 130 135 140

 gcc agc taa 441
 Ala Ser
 145

<210> 32
 <211> 146
 <212> PRT
 <213> M.Tuberculosis

<400> 32
 Met Pro Val Leu Ser Lys Thr Val Glu Val Thr Ala Asp Ala Ala Ser
 1 5 10 15
 Ile Met Ala Ile Val Ala Asp Ile Glu Arg Tyr Pro Glu Trp Asn Glu
 20 25 30
 Gly Val Lys Gly Ala Trp Val Leu Ala Arg Tyr Asp Asp Gly Arg Pro
 35 40 45
 Ser Gln Val Arg Leu Asp Thr Ala Val Gln Gly Ile Glu Gly Thr Tyr
 50 55 60
 Ile His Ala Val Tyr Tyr Pro Gly Glu Asn Gln Ile Gln Thr Val Met
 65 70 75 80
 Gln Gln Gly Glu Leu Phe Ala Lys Gln Glu Gln Leu Phe Ser Val Val
 85 90 95
 Ala Thr Gly Ala Ala Ser Leu Leu Thr Val Asp Met Asp Val Gln Val
 100 105 110
 Thr Met Pro Val Pro Glu Pro Met Val Lys Met Leu Leu Asn Asn Val
 115 120 125
 Leu Glu His Leu Ala Glu Asn Leu Lys Gln Arg Ala Glu Gln Leu Ala

130
 Ala Ser
 145

135

140

<210> 33
 <211> 894
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(891)

<400> 33

atg tca tcg ggc aat tca tct ctg gga att atc gtc ggg atc gac gat 48
 Met Ser Ser Gly Asn Ser Ser Leu Gly Ile Ile Val Gly Ile Asp Asp
 1 5 10 15

tca ccg gcc gca cag gtt gcg gtg cgg tgg gca gct cgg gat gcg gag 96
 Ser Pro Ala Ala Gln Val Ala Val Arg Trp Ala Ala Arg Asp Ala Glu
 20 25 30

ttg cga aaa atc cct ctg acg ctc gtg cac gcg gtg tcg ccg gaa gta 144
 Leu Arg Lys Ile Pro Leu Thr Leu Val His Ala Val Ser Pro Glu Val
 35 40 45

gcc acc tgg ctg gag gtg cca ctg ccg ccg ggc gtg ctg cga tgg cag 192
 Ala Thr Trp Leu Glu Val Pro Leu Pro Pro Gly Val Leu Arg Trp Gln
 50 55 60

cag gat cac ggg cgc cac ctg atc gac gac gca ctc aag gtg gtt gaa 240
 Gln Asp His Gly Arg His Leu Ile Asp Asp Ala Leu Lys Val Val Glu
 65 70 75 80

cag gct tcg ctg cgc gct ggt ccc ccc acg gtc cac agt gaa atc gtt 288
 Gln Ala Ser Leu Arg Ala Gly Pro Pro Thr Val His Ser Glu Ile Val
 85 90 95

ccg gcg gca gcc gtt ccc aca ttg gtc gac atg tcc aaa gac gca gtg 336
 Pro Ala Ala Ala Val Pro Thr Leu Val Asp Met Ser Lys Asp Ala Val
 100 105 110

ctg atg gtc gtg ggt tgt ctc gga agt ggg cgg tgg ccg ggc cgg ctg 384
 Leu Met Val Val Gly Cys Leu Gly Ser Gly Arg Trp Pro Gly Arg Leu
 115 120 125

ctc ggt tcg gtc agt tcc ggc ctg ctc cgc cac gcg cac tgt ccg gtc 432
 Leu Gly Ser Val Ser Ser Gly Leu Leu Arg His Ala His Cys Pro Val
 130 135 140

gtg atc atc cac gac gaa gat tcg gtg atg ccg cat ccc cag caa gcg 480
 Val Ile Ile His Asp Glu Asp Ser Val Met Pro His Pro Gln Gln Ala
 145 150 155 160

ccg gtg cta gtt ggc gtt gac ggc tcg tcg gcc tcc gag ctg gcg acc 528
 Pro Val Leu Val Gly Val Asp Gly Ser Ser Ala Ser Glu Leu Ala Thr
 165 170 175

gca atc gca ttc gac gaa gcg tcg cgg cga aac gtg gac ctg gtg gcg 576
 Ala Ile Ala Phe Asp Glu Ala Ser Arg Arg Asn Val Asp Leu Val Ala
 180 185 190

ctg cac gca tgg agc gac gtc gat gtg tcg gag tgg ccc gga atc gat 624
 Leu His Ala Trp Ser Asp Val Asp Val Ser Glu Trp Pro Gly Ile Asp
 195 200 205

 tgg ccg gca act cag tcg atg gcc gag cag gtg ctg gcc gag cgg ttg 672
 Trp Pro Ala Thr Gln Ser Met Ala Glu Gln Val Leu Ala Glu Arg Leu
 210 215 220

 gcg ggt tgg cag gag cgg tat ccc aac gta gcc ata acc cgc gtg gtg 720
 Ala Gly Trp Gln Glu Arg Tyr Pro Asn Val Ala Ile Thr Arg Val Val
 225 230 235 240

 gtg cgc gat cag ccg gcc cgc cag ctc gtc caa cgc tcc gag gaa gcc 768
 Val Arg Asp Gln Pro Ala Arg Gln Leu Val Gln Arg Ser Glu Glu Ala
 245 250 255

 cag ctg gtc gtg gtc ggc agc cgg ggc cgc ggc ggc tac gcc gga atg 816
 Gln Leu Val Val Val Gly Ser Arg Gly Arg Gly Gly Tyr Ala Gly Met
 260 265 270

 ctg gtg ggg tcg gta ggc gaa acc gtt gct cag ctg gcg cgg acg ccg 864
 Leu Val Gly Ser Val Gly Glu Thr Val Ala Gln Leu Ala Arg Thr Pro
 275 280 285

 gtc atc gtg gca cgc gag tcg ctg act tag 894
 Val Ile Val Ala Arg Glu Ser Leu Thr
 290 295

<210> 34
 <211> 297
 <212> PRT
 <213> M.Tuberculosis

<400> 34
 Met Ser Ser Gly Asn Ser Ser Leu Gly Ile Ile Val Gly Ile Asp Asp
 1 5 10 15
 Ser Pro Ala Ala Gln Val Ala Val Arg Trp Ala Ala Arg Asp Ala Glu
 20 25 30
 Leu Arg Lys Ile Pro Leu Thr Leu Val His Ala Val Ser Pro Glu Val
 35 40 45
 Ala Thr Trp Leu Glu Val Pro Leu Pro Pro Gly Val Leu Arg Trp Gln
 50 55 60
 Gln Asp His Gly Arg His Leu Ile Asp Asp Ala Leu Lys Val Val Glu
 65 70 75 80
 Gln Ala Ser Leu Arg Ala Gly Pro Pro Thr Val His Ser Glu Ile Val
 85 90 95
 Pro Ala Ala Ala Val Pro Thr Leu Val Asp Met Ser Lys Asp Ala Val
 100 105 110
 Leu Met Val Val Gly Cys Leu Gly Ser Gly Arg Trp Pro Gly Arg Leu
 115 120 125
 Leu Gly Ser Val Ser Ser Gly Leu Leu Arg His Ala His Cys Pro Val
 130 135 140
 Val Ile Ile His Asp Glu Asp Ser Val Met Pro His Pro Gln Gln Ala
 145 150 155 160
 Pro Val Leu Val Gly Val Asp Gly Ser Ser Ala Ser Glu Leu Ala Thr
 165 170 175
 Ala Ile Ala Phe Asp Glu Ala Ser Arg Arg Asn Val Asp Leu Val Ala
 180 185 190
 Leu His Ala Trp Ser Asp Val Asp Val Ser Glu Trp Pro Gly Ile Asp

	195		200		205										
Trp	Pro	Ala	Thr	Gln	Ser	Met	Ala	Glu	Gln	Val	Leu	Ala	Glu	Arg	Leu
	210					215					220				
Ala	Gly	Trp	Gln	Glu	Arg	Tyr	Pro	Asn	Val	Ala	Ile	Thr	Arg	Val	Val
225					230					235					240
Val	Arg	Asp	Gln	Pro	Ala	Arg	Gln	Leu	Val	Gln	Arg	Ser	Glu	Glu	Ala
			245					250					255		
Gln	Leu	Val	Val	Val	Gly	Ser	Arg	Gly	Arg	Gly	Gly	Tyr	Ala	Gly	Met
			260					265					270		
Leu	Val	Gly	Ser	Val	Gly	Glu	Thr	Val	Ala	Gln	Leu	Ala	Arg	Thr	Pro
		275					280					285			
Val	Ile	Val	Ala	Arg	Glu	Ser	Leu	Thr							
	290					295									

<210> 35
 <211> 957
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(954)

<400> 35																
atg	gct	gaa	gta	ctg	gtg	ctc	gtt	gag	cac	gct	gaa	ggc	gcg	tta	aag	48
Met	Ala	Glu	Val	Leu	Val	Leu	Val	Glu	His	Ala	Glu	Gly	Ala	Leu	Lys	
1				5					10					15		
aag gtc agc gcc gaa ttg atc acc gcc gcc cgc gcc ttg ggc gaa cca																96
Lys	Val	Ser	Ala	Glu	Leu	Ile	Thr	Ala	Ala	Arg	Ala	Leu	Gly	Glu	Pro	
			20					25					30			
gcc gcc gtc gtc gtc ggt gtg ccg ggg acg gcc gcg ccg ctg gtg gac																144
Ala	Ala	Val	Val	Val	Gly	Val	Pro	Gly	Thr	Ala	Ala	Pro	Leu	Val	Asp	
			35				40					45				
ggg ctt aag gcg gct ggt gcc gcc aag atc tac gtc gcc gag tcc gac																192
Gly	Leu	Lys	Ala	Ala	Gly	Ala	Ala	Lys	Ile	Tyr	Val	Ala	Glu	Ser	Asp	
	50					55					60					
ctt gtc gac aaa tac ctg atc acc ccg gcg gtc gac gtg ctg gcc ggg																240
Leu	Val	Asp	Lys	Tyr	Leu	Ile	Thr	Pro	Ala	Val	Asp	Val	Leu	Ala	Gly	
	65				70					75					80	
ctg gcc gag tcc tcg gcc cct gcc ggc gta cta atc gcc gcc acc gcg																288
Leu	Ala	Glu	Ser	Ser	Ala	Pro	Ala	Gly	Val	Leu	Ile	Ala	Ala	Thr	Ala	
			85					90						95		
gac ggc aag gag atc gcc ggc cga ctt gcg gct cgg atc ggc tcg ggt																336
Asp	Gly	Lys	Glu	Ile	Ala	Gly	Arg	Leu	Ala	Ala	Arg	Ile	Gly	Ser	Gly	
			100					105					110			
ctg ctg gtc gac gtg gtc gac gtg aga gaa ggt gga gtg ggt gtc cac																384
Leu	Leu	Val	Asp	Val	Val	Asp	Val	Arg	Glu	Gly	Gly	Val	Gly	Val	His	
			115				120					125				
agc atc ttc ggt ggg gcg ttc acc gtc gaa gcg cag gcc aac ggc gac																432
Ser	Ile	Phe	Gly	Gly	Ala	Phe	Thr	Val	Glu	Ala	Gln	Ala	Asn	Gly	Asp	
	130					135					140					
acc ccg gtg atc acc gtg cgc gca gga gcc gtg gag gcg gag ccg gcc																480

Thr Pro Val Ile Thr Val Arg Ala Gly Ala Val Glu Ala Glu Pro Ala
 145 150 155 160
 gcc ggc gcc ggt gag cag gtc agc gtg gaa gtg ccg gct gcg gcg gag 528
 Ala Gly Ala Gly Glu Gln Val Ser Val Glu Val Pro Ala Ala Ala Glu
 165 170 175
 aac gcc gcc agg atc acc gcg cgc gaa ccg gcg gtc gcc ggc gac cgg 576
 Asn Ala Ala Arg Ile Thr Ala Arg Glu Pro Ala Val Ala Gly Asp Arg
 180 185 190
 ccg gag ctg acc gag gcg acc att gtg gtg gcc ggt ggc cgt ggt gtc 624
 Pro Glu Leu Thr Glu Ala Thr Ile Val Val Ala Gly Gly Arg Gly Val
 195 200 205
 ggc agc gcg gag aac ttc agc gtg gtc gag gcg ctg gcc gac tcg ctg 672
 Gly Ser Ala Glu Asn Phe Ser Val Val Glu Ala Leu Ala Asp Ser Leu
 210 215 220
 ggc gcc gcg gtc ggg gcc tcg cgt gcc gca gtc gac tcc ggc tac tac 720
 Gly Ala Ala Val Gly Ala Ser Arg Ala Ala Val Asp Ser Gly Tyr Tyr
 225 230 235 240
 ccg ggc cag ttc cag gtc ggc cag acc ggc aag acg gtg tcg ccc cag 768
 Pro Gly Gln Phe Gln Val Gly Gln Thr Gly Lys Thr Val Ser Pro Gln
 245 250 255
 ctc tac att gcc ctg ggc atc tcc ggg gcg atc cag cac cgc gct ggc 816
 Leu Tyr Ile Ala Leu Gly Ile Ser Gly Ala Ile Gln His Arg Ala Gly
 260 265 270
 atg cag acg tcc aag acc atc gtc gcg gtc aac aag gac gaa gag gcg 864
 Met Gln Thr Ser Lys Thr Ile Val Ala Val Asn Lys Asp Glu Glu Ala
 275 280 285
 ccg atc ttt gag atc gcc gac tac ggg gtg gtg gga gac ctg ttc aag 912
 Pro Ile Phe Glu Ile Ala Asp Tyr Gly Val Val Gly Asp Leu Phe Lys
 290 295 300
 gtc gct ccg cag ctg acc gag gcc atc aag gcc cgc aag ggc 954
 Val Ala Pro Gln Leu Thr Glu Ala Ile Lys Ala Arg Lys Gly
 305 310 315
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 20 25 30
 Ala Ala Val Val Val Gly Val Pro Gly Thr Ala Ala Pro Leu Val Asp
 35 40 45
 Gly Leu Lys Ala Ala Gly Ala Ala Lys Ile Tyr Val Ala Glu Ser Asp
 50 55 60
 Leu Val Asp Lys Tyr Leu Ile Thr Pro Ala Val Asp Val Leu Ala Gly
 65 70 75 80

Leu Ala Glu Ser Ser Ala Pro Ala Gly Val Leu Ile Ala Ala Thr Ala
 85 90 95
 Asp Gly Lys Glu Ile Ala Gly Arg Leu Ala Ala Arg Ile Gly Ser Gly
 100 105 110
 Leu Leu Val Asp Val Val Asp Val Arg Glu Gly Gly Val Gly Val His
 115 120 125
 Ser Ile Phe Gly Gly Ala Phe Thr Val Glu Ala Gln Ala Asn Gly Asp
 130 135 140
 Thr Pro Val Ile Thr Val Arg Ala Gly Ala Val Glu Ala Glu Pro Ala
 145 150 155 160
 Ala Gly Ala Gly Glu Gln Val Ser Val Glu Val Pro Ala Ala Ala Glu
 165 170 175
 Asn Ala Ala Arg Ile Thr Ala Arg Glu Pro Ala Val Ala Gly Asp Arg
 180 185 190
 Pro Glu Leu Thr Glu Ala Thr Ile Val Val Ala Gly Gly Arg Gly Val
 195 200 205
 Gly Ser Ala Glu Asn Phe Ser Val Val Glu Ala Leu Ala Asp Ser Leu
 210 215 220
 Gly Ala Ala Val Gly Ala Ser Arg Ala Ala Val Asp Ser Gly Tyr Tyr
 225 230 235 240
 Pro Gly Gln Phe Gln Val Gly Gln Thr Gly Lys Thr Val Ser Pro Gln
 245 250 255
 Leu Tyr Ile Ala Leu Gly Ile Ser Gly Ala Ile Gln His Arg Ala Gly
 260 265 270
 Met Gln Thr Ser Lys Thr Ile Val Ala Val Asn Lys Asp Glu Glu Ala
 275 280 285
 Pro Ile Phe Glu Ile Ala Asp Tyr Gly Val Val Gly Asp Leu Phe Lys
 290 295 300
 Val Ala Pro Gln Leu Thr Glu Ala Ile Lys Ala Arg Lys Gly
 305 310 315

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 Val Lys Ser Thr Val Glu Gln Leu Ser Pro Thr Arg Val Arg Ile Asn
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 gtg gag gtg cca ttc gcc gag ctt gag ccg gat ttc cag cgg gcc tac 96
 Val Glu Val Pro Phe Ala Glu Leu Glu Pro Asp Phe Gln Arg Ala Tyr
 20 25 30
 aaa gag ctg gcc aaa cag gtg cgg ctg ccc ggc ttc cgg ccc ggg aag 144
 Lys Glu Leu Ala Lys Gln Val Arg Leu Pro Gly Phe Arg Pro Gly Lys
 35 40 45
 gcg ccg gcc aaa cta ctc gaa gcc cgc atc ggc cgg gag gcc atg ctg 192
 Ala Pro Ala Lys Leu Leu Glu Ala Arg Ile Gly Arg Glu Ala Met Leu
 50 55 60
 gat caa atc gtc aac gat gcg ctg ccc agc cgg tac gga cag gcg gtg 240
 Asp Gln Ile Val Asn Asp Ala Leu Pro Ser Arg Tyr Gly Gln Ala Val
 65 70 75 80

gcc gag tcg gat gtc caa ccg ctc ggc cgg ccc aac atc gag gtg acc Ala Glu Ser Asp Val Gln Pro Leu Gly Arg Pro Asn Ile Glu Val Thr 85 90 95	288
aag aag gag tac ggc cag gac ctg caa ttc acc gcc gag gtc gac atc Lys Lys Glu Tyr Gly Gln Asp Leu Gln Phe Thr Ala Glu Val Asp Ile 100 105 110	336
cgc ccg aag atc agt ccc ccg gac ctg agc gcg ctg acg gtc tcg gtg Arg Pro Lys Ile Ser Pro Pro Asp Leu Ser Ala Leu Thr Val Ser Val 115 120 125	384
gat ccg atc gaa atc ggt gag gac gac gtc gac gcc gaa ctg cag tcg Asp Pro Ile Glu Ile Gly Glu Asp Asp Val Asp Ala Glu Leu Gln Ser 130 135 140	432
tta cgt acc cgg ttc ggc acc ctg acc gcg gtg gac cgg ccg gtg gcc Leu Arg Thr Arg Phe Gly Thr Leu Thr Ala Val Asp Arg Pro Val Ala 145 150 155 160	480
gtc ggc gac gtc gtc tcg atc gac ttg tct gcc acg gtc gac gga gag Val Gly Asp Val Val Ser Ile Asp Leu Ser Ala Thr Val Asp Gly Glu 165 170 175	528
gac ata ccg aac gca gcc gct gag gga ctc tcc cac gag gtc ggc tcc Asp Ile Pro Asn Ala Ala Ala Glu Gly Leu Ser His Glu Val Gly Ser 180 185 190	576
ggc cgg ctc atc gca ggt ctc gac gac gcg gtt gtt ggt ctg tcc gcc Gly Arg Leu Ile Ala Gly Leu Asp Asp Ala Val Val Gly Leu Ser Ala 195 200 205	624
gac gag tcc cgg gtc ttc acc gcc aag ctg gca gcc ggc gag cac gcc Asp Glu Ser Arg Val Phe Thr Ala Lys Leu Ala Ala Gly Glu His Ala 210 215 220	672
ggg cag gaa gct cag gtt acc gtc acg gtc agg tcg gtt aag gag cgc Gly Gln Glu Ala Gln Val Thr Val Thr Val Arg Ser Val Lys Glu Arg 225 230 235 240	720
gaa cta cca gag ccc gac gac gaa ttc gcg cag tta gcc agc gag ttc Glu Leu Pro Glu Pro Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe 245 250 255	768
gac agc atc gac gaa ttg cgg gcc agc ctc agc gac cag gtg cgc cag Asp Ser Ile Asp Glu Leu Arg Ala Ser Leu Ser Asp Gln Val Arg Gln 260 265 270	816
gcc aag cgc gcc cag cag gcc gag cag att cga aac gcc acc atc gat Ala Lys Arg Ala Gln Gln Ala Glu Gln Ile Arg Asn Ala Thr Ile Asp 275 280 285	864
gcg cta ctc gaa cag gtc gac gtg ccg ttg ccg gag tcg tat gtg cag Ala Leu Leu Glu Gln Val Asp Val Pro Leu Pro Glu Ser Tyr Val Gln 290 295 300	912
gcc caa ttc gac agc gtg ctg cac agc gcg ctc agc ggt ctt aat cac Ala Gln Phe Asp Ser Val Leu His Ser Ala Leu Ser Gly Leu Asn His 305 310 315 320	960
gac gaa gcc cgg ttc aat gag ttg ctc gtc gag caa ggc tcg tca cgc	1008

Asp	Glu	Ala	Arg	Phe	Asn	Glu	Leu	Leu	Val	Glu	Gln	Gly	Ser	Ser	Arg		
				325					330						335		
gcg	gcg	ttc	gat	gcc	gag	gcg	cgc	acc	gcc	tca	gaa	aag	gac	gtc	aag		1056
Ala	Ala	Phe	Asp	Ala	Glu	Ala	Arg	Thr	Ala	Ser	Glu	Lys	Asp	Val	Lys		
			340					345					350				
agg	cag	ctg	ttg	cta	gac	gcc	ctg	gcc	gat	gag	ctg	cag	gtc	caa	gtt		1104
Arg	Gln	Leu	Leu	Leu	Asp	Ala	Leu	Ala	Asp	Glu	Leu	Gln	Val	Gln	Val		
		355					360					365					
ggc	cag	gat	gat	ctg	acc	gaa	cga	ctg	gtg	acg	acg	tct	cgg	caa	tac		1152
Gly	Gln	Asp	Asp	Leu	Thr	Glu	Arg	Leu	Val	Thr	Thr	Ser	Arg	Gln	Tyr		
	370					375					380						
ggc	atc	gag	ccg	cag	cag	ctg	ttc	ggc	tac	ctc	caa	gag	cgc	aac	cag		1200
Gly	Ile	Glu	Pro	Gln	Gln	Leu	Phe	Gly	Tyr	Leu	Gln	Glu	Arg	Asn	Gln		
385					390				395					400			
ctg	ccg	acc	atg	ttc	gct	gac	gtg	cgg	cgc	gag	ctg	gcg	atc	agg	gcc		1248
Leu	Pro	Thr	Met	Phe	Ala	Asp	Val	Arg	Arg	Glu	Leu	Ala	Ile	Arg	Ala		
				405				410						415			
gca	gtg	gag	gcg	gcg	acg	gtc	acc	gac	agt	gac	gga	aac	acg	atc	gat		1296
Ala	Val	Glu	Ala	Ala	Thr	Val	Thr	Asp	Ser	Asp	Gly	Asn	Thr	Ile	Asp		
			420					425					430				
acc	agt	gag	ttc	ttc	ggc	aag	cgt	gtg	tcg	gcc	ggt	gag	gct	gag	gag		1344
Thr	Ser	Glu	Phe	Phe	Gly	Lys	Arg	Val	Ser	Ala	Gly	Glu	Ala	Glu	Glu		
		435					440					445					
gcc	gaa	ccg	gca	gac	gag	ggc	gcc	gcg	cgg	gcg	gcg	tcc	gac	gaa	gcg		1392
Ala	Glu	Pro	Ala	Asp	Glu	Gly	Ala	Ala	Arg	Ala	Ala	Ser	Asp	Glu	Ala		
	450					455				460							
aca	acg	tga															1401
Thr	Thr																
465																	

<210> 38

<211> 466

<212> PRT

<213> M.Tuberculosis

<400> 38

Met	Lys	Ser	Thr	Val	Glu	Gln	Leu	Ser	Pro	Thr	Arg	Val	Arg	Ile	Asn		
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Val	Glu	Val	Pro	Phe	Ala	Glu	Leu	Glu	Pro	Asp	Phe	Gln	Arg	Ala	Tyr		
			20					25					30				
Lys	Glu	Leu	Ala	Lys	Gln	Val	Arg	Leu	Pro	Gly	Phe	Arg	Pro	Gly	Lys		
	35						40					45					
Ala	Pro	Ala	Lys	Leu	Leu	Glu	Ala	Arg	Ile	Gly	Arg	Glu	Ala	Met	Leu		
	50					55					60						
Asp	Gln	Ile	Val	Asn	Asp	Ala	Leu	Pro	Ser	Arg	Tyr	Gly	Gln	Ala	Val		
65				70						75					80		
Ala	Glu	Ser	Asp	Val	Gln	Pro	Leu	Gly	Arg	Pro	Asn	Ile	Glu	Val	Thr		
			85					90						95			
Lys	Lys	Glu	Tyr	Gly	Gln	Asp	Leu	Gln	Phe	Thr	Ala	Glu	Val	Asp	Ile		
			100				105						110				
Arg	Pro	Lys	Ile	Ser	Pro	Pro	Asp	Leu	Ser	Ala	Leu	Thr	Val	Ser	Val		

115 120 125
 Asp Pro Ile Glu Ile Gly Glu Asp Asp Val Asp Ala Glu Leu Gln Ser
 130 135 140
 Leu Arg Thr Arg Phe Gly Thr Leu Thr Ala Val Asp Arg Pro Val Ala
 145 150 155 160
 Val Gly Asp Val Val Ser Ile Asp Leu Ser Ala Thr Val Asp Gly Glu
 165 170 175
 Asp Ile Pro Asn Ala Ala Ala Glu Gly Leu Ser His Glu Val Gly Ser
 180 185 190
 Gly Arg Leu Ile Ala Gly Leu Asp Asp Ala Val Val Gly Leu Ser Ala
 195 200 205
 Asp Glu Ser Arg Val Phe Thr Ala Lys Leu Ala Ala Gly Glu His Ala
 210 215 220
 Gly Gln Glu Ala Gln Val Thr Val Thr Val Arg Ser Val Lys Glu Arg
 225 230 235 240
 Glu Leu Pro Glu Pro Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe
 245 250 255
 Asp Ser Ile Asp Glu Leu Arg Ala Ser Leu Ser Asp Gln Val Arg Gln
 260 265 270
 Ala Lys Arg Ala Gln Gln Ala Glu Gln Ile Arg Asn Ala Thr Ile Asp
 275 280 285
 Ala Leu Glu Glu Gln Val Asp Val Pro Leu Pro Glu Ser Tyr Val Gln
 290 295 300
 Ala Gln Phe Asp Ser Val Leu His Ser Ala Leu Ser Gly Leu Asn His
 305 310 315 320
 Asp Glu Ala Arg Phe Asn Glu Leu Leu Val Glu Gln Gly Ser Ser Arg
 325 330 335
 Ala Ala Phe Asp Ala Glu Ala Arg Thr Ala Ser Glu Lys Asp Val Lys
 340 345 350
 Arg Gln Leu Leu Leu Asp Ala Leu Ala Asp Glu Leu Gln Val Gln Val
 355 360 365
 Gly Gln Asp Asp Leu Thr Glu Arg Leu Val Thr Thr Ser Arg Gln Tyr
 370 375 380
 Gly Ile Glu Pro Gln Gln Leu Phe Gly Tyr Leu Gln Glu Arg Asn Gln
 385 390 395 400
 Leu Pro Thr Met Phe Ala Asp Val Arg Arg Glu Leu Ala Ile Arg Ala
 405 410 415
 Ala Val Glu Ala Ala Thr Val Thr Asp Ser Asp Gly Asn Thr Ile Asp
 420 425 430
 Thr Ser Glu Phe Phe Gly Lys Arg Val Ser Ala Gly Glu Ala Glu Glu
 435 440 445
 Ala Glu Pro Ala Asp Glu Gly Ala Ala Arg Ala Ala Ser Asp Glu Ala
 450 455 460
 Thr Thr
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 <212> PRT
 <213> M.Tuberculosis

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 1 5 10 15

<210> 40
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<400> 40

Thr Asp Thr Gln Val Thr Trp Leu Thr Gln Glu Ser His Asp Arg
 1 5 10 15

<210> 41
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 <213> M.Tuberculosis

<400> 41

Met Ile Asp Glu Ala Leu Phe Asp Ala Glu Glu Lys Met Glu Lys
 1 5 10 15

<210> 42
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<400> 42

Pro Leu Pro Ala Asp Pro Ser Thr Asp Leu Ser Ala Tyr Ala Gln
 1 5 10 15

<210> 43
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<400> 43

Met Leu Ile Ser Gln Arg Pro Thr Leu Ser Glu Asp Val Leu Thr
 1 5 10 15

<210> 44
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 <213> M.Tuberculosis

<400> 44

Thr Gly Asn Leu Val Thr Lys Asn Ser Leu Thr Pro Asp Val Arg
 1 5 10 15

<210> 45
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 <213> M.Tuberculosis

<400> 45

Met Glu Val Lys Ile Gly Ile Thr Asp Ser Pro Arg Glu Leu Val
 1 5 10 15

<210> 46
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 <212> PRT
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<400> 46

Ser Ala Tyr Lys Thr Val Val Val Gly Thr Asp Asp Xaa Ser Xaa
 1 5 10 15

<210> 47
 <211> 15
 <212> PRT
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<400> 47

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<210> 48

<211> 15

<212> PRT

<213> M.Tuberculosis

<400> 48

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<210> 49

<211> 15

<212> PRT

<213> M.Tuberculosis

<400> 49

Thr	Tyr	Glu	Thr	Ile	Leu	Val	Glu	Arg	Asp	Gln	Arg	Val	Gly	Ile
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<210> 50

<211> 15

<212> PRT

<213> M.Tuberculosis

<400> 50

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<210> 51

<211> 14

<212> PRT

<213> M.Tuberculosis

<400> 51

Pro	Val	Val	Lys	Ile	Asn	Ala	Ile	Glu	Val	Pro	Ala	Gly	Ala
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<210> 52

<211> 15

<212> PRT

<213> M.Tuberculosis

<400> 52

Ala	Asp	Lys	Thr	Thr	Gln	Thr	Ile	Tyr	Ile	Asp	Ala	Asp	Pro	Gly
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<210> 53

<211> 15

<212> PRT

<213> M.Tuberculosis

<400> 53

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<210> 54

<211> 14

<212> PRT
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1 5 10 15

<210> 56
<211> 15
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<400> 56
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1 5 10 15

<210> 57
<211> 11
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<400> 57
Val Ile Arg Arg Lys Pro Lys Pro Arg Xaa Arg
1 5 10

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<212> DNA
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<400> 59
ctcccatggc tacttaccg ctcgtagcaa c 31

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<400> 60
ctgagatctc ctgtcactca ggaagaa 27

<210> 61
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<400> 61
ctcccatggg aaaccgccat tagcggg 27

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cccaagctta tggaacagcg tgcggag 27

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<400> 63
ctcccatggc gacactcgat ccggatt 27

<210> 64
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ctgagatcta tgccagtggg gaagatc 27

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<400> 65
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<210> 67
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<400> 67
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<210> 68
<211> 27
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<400> 68
ctgagatctc cagttttgag caagacc 27

<210> 69
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<400> 69
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<210> 70
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<400> 70
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<210> 71
 <211> 31
 <212> DNA
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<400> 71
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<210> 72
 <211> 27
 <212> DNA
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<400> 72
 ctgagatctg tgaagagcac cgtcgag 27

<210> 73
 <211> 27
 <212> DNA
 <213> M.Tuberculosis

<400> 73
 ctcccatggg tcatacggtc acgttgt 27

<210> 74
 <211> 348
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(348)

<400> 74
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 1 5 10 15

aag ctt gcc ggc tgg tgg gcc gag cag ttc gat ggc acg acg cgt gaa 96
 Lys Leu Ala Gly Trp Trp Ala Glu Gln Phe Asp Gly Thr Thr Arg Glu
 20 25 30

ctg ctg ccc gcc gaa ttc gtc gtg gtc gcc cgg acc gat gga ccg cgg 144
 Leu Leu Pro Gly Glu Phe Val Val Val Ala Arg Thr Asp Gly Pro Arg

35	40	45	
ttg gga ttc cag aag gtg ccc gat ccc gcc cct ggg aaa aac cgc gtg			192
Leu Gly Phe Gln Lys Val Pro Asp Pro Ala Pro Gly Lys Asn Arg Val			
50	55	60	
cac ctc gac ttc acg acc aag gac ctg gat gcc gag gtg ttg cgc ctg			240
His Leu Asp Phe Thr Thr Lys Asp Leu Asp Ala Glu Val Leu Arg Leu			
65	70	75	80
gtc gcc gcc gga gcc agt gag gtc ggg cgg cat cag gtc ggc gag agc			288
Val Ala Ala Gly Ala Ser Glu Val Gly Arg His Gln Val Gly Glu Ser			
	85	90	95
ttt cgc tgg gtg gtg ctg gct gac ccc gaa ggc aac gct ttt tgc gtg			336
Phe Arg Trp Val Val Leu Ala Asp Pro Glu Gly Asn Ala Phe Cys Val			
	100	105	110
gcg ggt caa taa			348
Ala Gly Gln *			
	115		

<210> 75
 <211> 115
 <212> PRT
 <213> M.Tuberculosis

<400> 75
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 Leu Leu Pro Gly Glu Phe Val Val Ala Arg Thr Asp Gly Pro Arg
 35 40 45
 Leu Gly Phe Gln Lys Val Pro Asp Pro Ala Pro Gly Lys Asn Arg Val
 50 55 60
 His Leu Asp Phe Thr Thr Lys Asp Leu Asp Ala Glu Val Leu Arg Leu
 65 70 75 80
 Val Ala Ala Gly Ala Ser Glu Val Gly Arg His Gln Val Gly Glu Ser
 85 90 95
 Phe Arg Trp Val Val Leu Ala Asp Pro Glu Gly Asn Ala Phe Cys Val
 100 105 110
 Ala Gly Gln
 115

<210> 76
 <211> 564
 <212> DNA
 <213> M.Tuberculosis

<220>
 <221> CDS
 <222> (1)...(564)

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 Met Ala Asp Ala Asp Thr Thr Asp Phe Asp Val Asp Ala Glu Ala Pro
 1 5 10 15
 ggt gga ggc gtc cgg gag gac acg gcg acg gat gct gac gag gcc gac
 96

Gly	Gly	Gly	Val	Arg	Glu	Asp	Thr	Ala	Thr	Asp	Ala	Asp	Glu	Ala	Asp		
			20					25					30				
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Asp	Gln	Glu	Glu	Arg	Leu	Val	Ala	Glu	Gly	Glu	Ile	Ala	Gly	Asp	Tyr		
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44

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C07K 14/35, A61K 39/04, G01N 33/569	A3	(11) International Publication Number: WO 00/21983 (43) International Publication Date: 20 April 2000 (20.04.00)
(21) International Application Number: PCT/DK99/00538 (22) International Filing Date: 8 October 1999 (08.10.99) (30) Priority Data: PA 1998 01281 8 October 1998 (08.10.98) DK 60/116,673 21 January 1999 (21.01.99) US (71) Applicant (for all designated States except US): STATENS SERUM INSTITUT [DK/DK]; Artillerivej 5, DK-2300 Copenhagen S (DK). (72) Inventors; and (75) Inventors/Applicants (for US only): ANDERSEN, Peter [DK/DK]; Sparreholmvej 47, DK-2700 Brønshøj (DK). WELDINGH, Karin [DK/DK]; Nørrebrogade 224, 3. tv, DK-2200 Copenhagen N (DK). HANSEN, Christina, Væggerby [DK/GB]; 14 Conyngham Road, Victoria Park, Manchester M14 5SA (GB). FLORIO, Walter [IT/IT]; Via Carriona, 226, I-Carrara (IT). OKKELS, Li, Mei, Meng [DK/DK]; Aldershvilevej 116A, DK-2880 Bagsværd (DK). SKJØT, Rikke, Louise, Vinther [DK/DK]; Thorvaldsensvej 9, 5. sal, DK-1871 Frederiksberg C (DK). ROSENKRANDS, Ida [DK/DK]; Kastaniehaven 9, DK-3500 Værløse (DK).		(74) Agent: PLOUGMANN, VINGTOFT & PARTNERS A/S; Sankt Annæ Plads 11, P.O. Box 3007, DK-1021 Copen- hagen (DK). (81) Designated States: AE, AL, AM, AT, AT (Utility model), AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, CZ (Utility model), DE, DE (Utility model), DK, DK (Utility model), DM, EE, EE (Utility model), ES, FI, FI (Utility model), GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK (Utility model), SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> (88) Date of publication of the international search report: 23 November 2000 (23.11.00)

(54) Title: TUBERCULOSIS VACCINE AND DIAGNOSTIC REAGENTS BASED ON ANTIGENS FROM THE *MYCOBACTERIUM TUBERCULOSIS* CELL

(57) Abstract

The present invention relates to substantially pure polypeptides, which has a sequence identity of at least 80 % to an amino acid sequence disclosed, or which is a subsequence of at least 6 amino acids thereof, preferably a B- or T-cell epitope of the polypeptides disclosed. The polypeptide or the subsequence thereof has at least one of nine properties. The use of the disclosed polypeptides in medicine is disclosed, preferably as vaccine or diagnostic agents relating to virulent *Mycobacterium*. The invention further relates to the nucleotide sequences disclosed and the nucleotide sequences encoding the disclosed polypeptides. Medical and non-medical use of the nucleotide sequences is disclosed.

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EE	Estonia	LR	Liberia	SG	Singapore		

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 7 C07K14/35 A61K39/04 G01N33/569

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 16646 A (CORIXA CORP) 23 April 1998 (1998-04-23) page 2, line 7 - line 14 page 4, line 14 - line 21 page 5, line 14 - line 21 SEQ IDNO 190, 195 page 28, line 16; example 30 abstract --- -/--	1-15, 18-23

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

17 April 2000

Date of mailing of the international search report

20. 09. 00

Name and mailing address of the ISA

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 Fax: (+31-70) 340-3016

Authorized officer

H. Nilsson

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X A	EIGIMEIER AT AL: "Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae" MOLECULAR MICROBIOLOGY, vol. 7, no. 2, 1993, pages 197-206, XP002900965 page 197 -page 205; figure 2 abstract	1-6 7-15, 18-23
P,X	--- COLE S T: "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence" NATURE, vol. 393, 11 June 1998 (1998-06-11), pages 537-544, XP002900966 abstract page 542, right-hand column, paragraph 2; table 1H	1-6
P,A	-----	7-15, 18-23

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 99/00538

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-15, 18-23

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK99/00538

According to PCT Rules 13.1 and 13.2, an international application shall relate to one invention only or a group of inventions linked by one or more of the same corresponding "special technical features", i.e. features that define a contribution which each of the inventions makes over the prior art.

In the present application the following inventions have been found *à posteriori* in relation to W098/16646:

1-22. Substantially pure polypeptides with a sequence identity of at least 80% to an amino acid disclosed in SEQ ID NOs 34, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 36, 38, 75, 77 and 79 respectively (each sequence corresponding to one invention) as well as nucleotide sequences coding disclosed in SEQ ID NOs 33, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 74, 76 and 78 encoding the polypeptides, which constitute 22 different inventions. These inventions also relate to the use of the polypeptides and nucleotide sequences and are disclosed in claims 1-15 and 18-23. Inventions 1-5 (sequences disclosed in SEQ ID NOs 34, 2, 4, 6, 8, and 33, 1, 3, 5, 7) have been searched.

23. An extract of polypeptides from Mycobacteria and the use of the extract for the preparation of a composition for the generation of an immune response against Mycobacterium. This invention is disclosed in claims 16-17 and has not been searched.

The special technical feature of each of the inventions 1-22 is each specific amino acid sequence. At least one of the searched sequences has been published in W098/16646 and is expected to have properties equal to the corresponding polypeptide of the application. The special technical feature of invention 23 is the extract of polypeptides obtained using a certain method. Thus, the inventions found in the application are not linked by any common special technical feature and the application lacks unity *à posteriori*.

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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		CZ 9901265 A	17-11-1999
		EP 0932681 A	04-08-1999
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